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OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 16:38:39 ; Search time 192.714 Seconds

(without alignments)
7926.909 Million cell updates/sec

Perfect score: 3461

Sequence: 1 ctctgtgcgaaatccggcaat aaattccttatatacgatcg 3461

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA : *

1: /cgn2_6/btodata/2/ina/5A_COMB.seq;*
2: /cgn2_6/btodata/2/ina/5B_COMB.seq;*
3: /cgn2_6/btodata/2/ina/6A_COMB.seq;*
4: /cgn2_6/btodata/2/ina/6B_COMB.seq;*
5: /cgn2_6/btodata/2/ina/pcrus_COMB.seq;*
6: /cgn2_6/btodata/2/ina/backfiles.seq;*

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2249	65.0	2404	1	US-08-311-023-3	Sequence 3, Appli
2	1288	37.2	1310	1	US-08-311-023-3	Sequence 1, Appli
3	360	10.4	385	4	US-09-712-016-78	Sequence 78, Appli
c	5	240	6.9	241	4	US-09-620-405-B-360
c	6	240	6.9	241	4	US-09-433-826B-360
c	7	240	6.9	241	4	US-09-433-826B-360
c	8	165	4.8	177	3	US-09-604-287A-160
c	9	165	4.8	177	3	US-09-020-955-162
c	10	165	4.8	177	4	US-09-030-607-162
c	11	165	4.8	177	4	US-09-429-313-162
c	12	110.6	4.8	177	4	US-09-352-616A-162
c	13	110.6	3.2	1888	4	US-09-233-149A-162
c	14	59.8	1.7	285	3	US-08-599-360B-38
c	15	59.8	1.7	285	4	US-08-990-571-64
c	16	59.8	1.7	285	4	US-09-528-78A-64
c	17	59.8	1.7	342	3	US-08-990-571-65
c	18	59.8	1.7	342	4	US-09-528-78A-65
c	19	59.8	1.7	342	4	US-09-569-098A-65
c	20	59.8	1.7	351	3	US-08-990-571-60
c	21	59.8	1.7	351	4	US-09-569-098A-60
c	22	59.8	1.7	356	3	US-08-990-571-63
c	23	59.8	1.7	356	4	US-09-569-098A-63
c	24	59.8	1.7	356	4	US-09-528-78A-63
c	25	59.8	1.7	356	4	US-09-569-098A-63
c	26	59.8	1.7	358	3	US-08-990-571-58
c	27	59.8	1.7	358	4	US-09-528-78A-58

Sequence 58, Appli
Sequence 66, Appli
Sequence 67, Appli
Sequence 66, Appli
Sequence 67, Appli
Sequence 66, Appli
Sequence 67, Appli
Sequence 59, Appli
Sequence 61, Appli
Sequence 61, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 5, Appli
Sequence 42, Appli

ALIGNMENTS

RESULT 1
US-08-311-023-3
; Sequence 3, Application US/08311023
; Patent No. 5693465
; GENERAL INFORMATION:
; APPLICANT: MANNING, David Lockwood
; APPLICANT: NICHOLSON, Robert Ian
; APPLICANT: GEE, Julia Margaret
; APPLICANT: GREEN, Christopher Douglas
; TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF BREAST TUMOURS
; TITLE OF INVENTION: BREAST TUMOURS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; CITY: 745 South 23rd Street
; STATE: VA
; ZIP: 22202
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.023
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: Reg. No. 5693465 32,925
; REFERENCE/DOCKET NUMBER: WCM.56
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/685-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-311-023-3
; Query Match Score 2249;
; Best Local Similarity 97.4%;
; Matches 63; Conservative 0; Mismatches 0; Indels 60;
; Gaps 3;
; QY 1119 GGTTTATGCCATTCCATCATGTTCCGGGTATACTAGTGCCT 1178

Db	1	GGTTTATAGCCATTCCATCATAGTTCCCTGCTGGGTTATCTGGCT	60	QY	2259	GAATGCTGCCACATGATGCTAGTGACCTATGGATGTGCCCTGGGGTATATTCCTTTTA	2318
QY	1179	CTCAGAACGCGGTGTTCAANTTCCTCCNAGTTGCGACTGCCGTGG	1238	Db	1141	GAATGCTGCCACATGATGCTAGTGACCTATGGATGTGCCCTGGGGTATATTCCTTTTA	1200
Db	61	CTCAGAACGCGGTGTTCAANTTCCTCCNAGTTGCGACTGCCGTGG	120	QY	2319	CAGATGCTGGATGGTGGTTGGGTTGGAAATTGGTACTATTCATATTGACAT	2378
QY	1239	ACTTGAGGGTGTGATGCTTACCCCTTCACATTCTCATGAAAGTACACCAT	1298	Db	1201	CAGATGCGGGATGGTGGTTGGGAAATTGGTACTATTCATATTGACAT	1259
Db	121	ACTTGAGGGTGTGATGCTTACCCCTTCACATTCTCATGAAAGTACACCAT	180	QY	2379	AAATGCTGGTTGCTGATAAATTCTTAGTTAATGCTAGTAGCTAAAGT	2438
QY	1299	AGTCATAGCATGATGAAAGCAGCAATTGCTAGTCATCTG	1358	Db	1260	AAATGCTGGTTGCTGATAAATTCTTAGTTAATGCTAGTAGCTAAAGT	1318
Db	181	AGTCATAGCATGATGAAAGCAGCAATTGCTAGTCATCTG	240	QY	2439	TGCTCATAGTTCTAGTAGCTAGTCATAGGAGATGACTTGTATGCTGFACTATGCAGCCTTA	2498
QY	1359	TCTPTCRAAADATAGAAAGCTGCTATTGTGATGAAAGCCTGCTAACACCT	1418	Db	1319	TGCTCATAGTTCTAGTAGCTAGTCATAGGAGATGACTTGTATGCTGFACTATGCAGCCTTA	1378
Db	241	TCTTTCARAAACATAGAAAGCAGCTGCTATTGTGATGAAAGCCTGTAACGCT	300	QY	2499	AAGTTAGTGGGTTTGTGATTGTTGATGAAATATTGCTGCTGCTGATGCTGTTAA	2558
QY	1419	CTAGGAGGCTGTTATTCATGTTCTGTGACATGCTCATGTCACACATT	1478	Db	1379	AAGTTAGTGGGTTTGTGATTGTTGATGAAATATTGCTGCTGATGCTGTTAA	1438
Db	301	CTAGGAGGCTGTTATTCATGTTCTGTGACATGCTCATGTCACACATT	360	QY	2559	AGTACGTTTAAATTAACTTCTGATGCTGAAACTCTGATGCTGAACTTCA	2618
QY	1479	AAAGTTAGAGAAAGATCAGAAACCTGAAATGATGATGATGTTGAGATTAG	1538	Db	1439	AGTACGTTTAAATTAACTTCTGATGCTGAAACTCTGATGCTGAACTTCA	1498
Db	361	AAAGTTAGAGAAAGATCAGAAACCTGAAATGATGATGTTGAGATTAG	420	QY	2619	CGGTTATGACCATTATGTTGATGACATGCTGTTGATGCTGTTAA	2678
QY	1539	AAGCAGTTGCTCAAAGTAACTTCACACTTCAACTTCAACTTCAACTTCA	1598	Db	1449	CCGGATATACCAGTTTATGCTTAACTGCTGTTGATGCTGTTGATGCTGTT	1558
Db	421	AAGCAGTTGCTCAAAGTAACTTCACACTTCAACTTCAACTTCAACTTCA	480	QY	2679	AGGGAAAATGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAA	2738
QY	1599	GATCCAACCTGAGGCTTAACTGAGCACTACAGAGCCTCCACTTGTGTCAG	1658	Db	1559	AGGAAAATGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAA	1618
Db	481	GATCCAACCTGAGGCTTAACTGAGCACTACAGCAAGCTCCACUTTCATCTG	540	QY	2739	TAGGCTCTGAGAACGCTGCTGTTGATGCTGAACTTAACTGCTGAACTTAA	2798
QY	1659	CAGCTGCACTTGTGAGAGAGGTCTGATGCTCATGCTCATCCACAGGAGTC	1718	Db	1619	TAGGCTCTGAGAACGCTGCTGTTGATGCTGAACTTAACTGCTGAACTTAA	1678
Db	541	CAGCTGCACTTGTGAGAGAGGTCTGATGCTCATGCTCATCCACAGGAGTC	600	QY	2799	AAGAAAGCTTATAGTAACTTAACTGAAAGAAATAAGGAGAAAGAGAACTGAGAA	2858
QY	1719	TACATGATGATATACCCAGGGTTCAGAAATAATGCCATTCAACATTCCAGATA	1778	Db	1679	AAGAAGCTTATAGTAACTTAACTGAAATAAGGAGAAATAAGGAGAACTGAGAA	1738
Db	601	TACATGATGATATACCCAGGGTTCAGAAATAATGCCATTCAACATTCCAGATA	660	QY	2859	TGGGGAGGCTGATGCTTAACTTAACTGAAATAAGGAGAAATAAGGAGAA	2918
QY	1779	CTCGCCAGTCAGAGATCTCATGACCACTCATGACCACTCATTCCTCCAT	1838	Db	1739	TGGGGAGGCTGATGCTTAACTTAACTGAAATAAGGAGAAATAAGGAGAA	1798
Db	661	CTCGCCAGTCAGAGATCTCATGACCACTCATGACCACTCATTCCTCCAT	720	QY	2919	TITAGATAAGATAAAAGCAGATAAGTAACTGACATTAACTTAACTTAACTTAA	2978
QY	1839	CACCAACCACCAACCCATCCTCACAGTCAGCCAGGCTACTCTGGAGGGCTG	1898	Db	1799	TITAGATAAGATAAAAGCAGATAAGTAACTGACATTAACTTAACTTAACTTAA	1858
Db	721	CACCAACCACCAACCCATCCTCACAGTCAGCCAGGCTACTCTGGAGGGCTG	780	QY	2979	CAGGATAATTCCCGTAAGAACGCTGACTCATACATACATACATACATACAT	3038
QY	1899	AAAGATGGGGCTGCTGAAATGCTGCTGATGTTGCTGATGGCTGCACTA	1958	Db	1859	CAGGATAATTCCCGTAAGAACGCTGACTCATACATACATACATACATACAT	1918
Db	781	AAAGATGGGGCTGCTGAAATGCTGCTGATGTTGCTGATGGCTGCACTA	840	QY	3039	AGGAAATGCAAACTTCAAAATTCATGAAATTCATGAAATTCATGAAATTC	3098
Db	901	ACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCACTA	960	QY	3159	TATGTTATACCCACTGGGTATGCTGCACTGTTATATCAACAAAGGTATGACTG	3218
QY	2019	CTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCACTA	2138	Db	2039	TATGTTATACCCACTGGGTATGCTGCACTGTTATATCAACAAAGGTATGACTG	2098
QY	961	CTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCACTA	1020	QY	3219	GATGTTGCTGTTACTCTGGTTACAAATATTGCTGATGCTGTTGCTGCTG	3258
Db	2139	GCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2198	Db	2099	GATGTTGCTGTTACTCTGGTTACAAATATTGCTGATGCTGTTGCTGCTG	2158
QY	1021	CGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080	QY	3259	-AAAATCTGATATATATGAG	3278
Db	2139	TGGTATTTGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2256	Db	2159	GATATTAACACTAACATAGTATCATTGCTGATTGCTGATTGCTGATTGCT	2218
QY	1081	TGGTATTTGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140	Db			

Page 3

RESULT 3
 US-09-712-016-78
 ; Sequence 78, Application US/09712016
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Giese, Klaus
 ; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER
 ; CURRENT APPLICATION NUMBER: US/09/712,016
 ; FILE REFERENCE: 200130_460
 ; CURRENT FILING DATE: 2000-11-13
 ; PRIORITY APPLICATION NUMBER: US/09/417,615
 ; PRIOR FILING DATE: PRIORITY FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 78
 ; LENGTH: 385
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; OTHER INFORMATION: n = A,T,C or G

Query Match 10.4%; Score 360; DB 4; Length 385;
 Best Local Similarity 98.2%; Pred. No. 1.3e-90;
 Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2453 TAGGTCAAGGGAGATGAGTTGTAACGTACTATGCACCGTTAAAGTGTAGTGGTT 2512
 Db 1 TCGGTCATGGAGA-GATTTGTAACGTACTATGCACCGTTAAAGTGTAGTGGTT 58

Query Match 10.4%; Score 360; DB 4; Length 385;
 Best Local Similarity 98.2%; Pred. No. 1.3e-90;
 Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2513 TGTGATTTGTATGATAATGGCTGTACAAGTCAGTTAACAGTAGTTTAAT 2572
 Db 59 TGTGATTTGTATGATAATGGCTGTACAAGTCAGTTAACAGTAGTTTAAT 118

QY 2573 ATTTAAGTATCTACCTTGAGATAAGATGGCTGATCACGTGTTAACGGATTACACT 2632
 Db 119 ATTTAAGTATCTACCTTGAGATAAGATGGCTGATCACGTGTTAACGGATTACACT 178

QY 2633 TTATTAATAAACAGAGATGGCTGATCACGTGTTAACGGAAAATGCT 2692
 Db 179 TTATTAATAAACAGAGATGGCTGATCACGTGTTAACGGAAAATGCT 238

QY 2693 TTATGCTTTCAAGAACTAACAGATGATGCTGATCACGTGTTAACGGATTAC 2752
 Db 239 TTATGCTTTCAAGAACTAACAGATGATGCTGATCACGTGTTAACGGATTAC 298

QY 2753 ACTCTGCTGTTAGAAATAGATGCTGATCACGTGTTAACGGATTAC 2812
 Db 299 ACTCTGCTGTTAGAAATAGATGCTGATCACGTGTTAACGGATTAC 358

QY 2813 TGATTTAGCAAGAAATAA 2834
 Db 359 TGATTTAGCAAGAAATAA 380

RESULT 4
 US-09-389-681-360/c
 ; Sequence 360, Application US/09389681A
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuqiu, Jiang
 ; APPLICANT: Dillon, Darvin C.
 ; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121_47053
 ; CURRENT APPLICATION NUMBER: US/09/389,681A
 ; CURRENT FILING DATE: 1999-09-02
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 360
 ; LENGTH: 241
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(241)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-389-681-360

Query Match 6.9%; Score 240; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 3.1e-57;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2720 TATTCCTATACGTGATTTAGGCTCTGAAGAACGCTGCTGTTAGGAAATAGATG 2779
 Db 241 TATTCCTATACGTGATTTAGGCTCTGAAGAACGCTGCTGTTAGGAAATAGATG 182

QY 2780 GCATGAACGCTAAATACCACAGAAAGCTTAACTGATTTAAGCTTAAGGAA 2839
 Db 181 GCATGAACGCTAAATACCACAGAAAGCTTAACTGATTTAAGGAAAGGAA 122

QY 2840 AAAGAGAAATCTGAGAATGGGAGGCTAGATCTTAAATCATCAAATTTGT 2899
 Db 121 AAAGAGAAATCTGAGAATGGGAGGCTAGATCTTAAATCATCAAATTTGT 62

RESULT 5
 US-09-020-405B-360/C
 ; Sequence 360, Application US/09620405B
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Jian, Yugu
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harlicker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121_470CB
 ; CURRENT APPLICATION NUMBER: US/09/620,405B
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 495
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 360
 ; LENGTH: 241
 ; TYPE: DNA
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(241)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-620-405B-360

Query Match 6.9%; Score 240; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 3.1e-57;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2720 TATTCCTATACGTGATTTAGGCTCTGAAGAACGCTGCTGTTAGGAAATAGATG 2779

Db 241 TATTCCTATCTGGATTAGTCTCTGAGAACCTGCTGGTTAGGATAAGAATGT 182
 Qy 2780 GCGAGGCCTAAATACCAAAACTTACAGAATTAGAAGAAATAAGGGA 2839
 Db 181 GCGAGGCCTAAATACCAAAACTTACAGAATTAGAAGAAATAAGGGA 122
 Qy 2840 AAGAGAGAATCTGAGATGGGAGCATAGATCTTAAATCACAATTT 2899
 Db 121 AAGAGAATCTGAGATGGGAGCATAGATCTTAAATCACAATTTGTT 62
 Qy 2900 GTAAATTAGAGGGAGAAATTAGATTAGTATAAAAAGGCAAGATTAGTATAGCTAC 2959
 Db 61 GTAAATTAGAGGGAGAAATTAGATTAGTATAAAAAGGCAAGATTAGTATAGCTAC 2

RESULT 6
 US-09-433-826B-360/c
 Sequence 360, Application US/09433826B
 Patent No. 657973
 GENERAL INFORMATION:
 APPLICANT: Jiang, Yuguil
 Dillion, Davin C.
 MITCHAM, Jennifer L.
 APPLICANT: Xu, Jiangchun
 Harlocker, Susan L.
 TITLE OF INVENTION: DIAGNOSTICS OF BREAST CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.470C4
 CURRENT APPLICATION NUMBER: US/09/433,826B
 CURRENT FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 474
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 360
 LENGTH: 241
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: (1)...(241)
 OTHER INFORMATION: n = A,T,C or G
 US-09-433-826B-360

Query Match 6.9%; Score 240; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 3..1e-57;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2720 TTATCCCTATCTGGATTAGTCTCTGAGAACCTGCTGGTTAGGATAAGAATGT 2779
 Db 241 TTATCCCTATCTGGATTAGTCTCTGAGAACCTGCTGGTTAGGATAAGAATGT 182
 Qy 2780 GCATGAGCCAAATACCAAAAGGAAAGCTTAACTGAAATTAGAAGAAATAAGGGA 2839
 Db 181 GCATGAGCCAAATACCAAAAGGAAAGCTTAACTGAAATTAGAAGAAATAAGGGA 122
 Qy 2840 AAAGAGAAATCTGAAATTGGGGCATAGATCTTAAATCACAATTTGTT 2899
 Db 121 AAAGAGAAATCTGAAATTGGGGCATAGATCTTAAATCACAATTTGTT 62
 Qy 2900 GTAAATTAGAGGGAGAAATTAGATTAGTATAAAAAGGCAAGATTAGTATAGCTAC 2959
 Db 61 GTAAATTAGAGGGAGAAATTAGATTAGTATAAAAAGGCAAGATTAGTATAGCTAC 2

RESULT 8
 US-09-020-956-162/c
 Sequence 162, Application US/09020956
 Patent No. 6261562
 GENERAL INFORMATION:
 APPLICANT: Dillin, Davin C.
 MITCHAM, Jennifer L.
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHOD:
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 ZIP: 98104
 COUNTRY: USA
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,956
 FILING DATE: 09-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mai, David J.
 PATENT NO.: 6585572
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-1900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 162:
 SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-020-956-162

Query Match Score 165; DB 3; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.2e-36;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3159 TTTATGTTACCAAGACTGGTTATGCCAAGTTATCACCAGCTATGCTATGACTG 3218
 Db 165 TTATGTTACCAAGACTGGTTATGCCAAGTTATCACCAGCTATGCTATGACTG 106

Qy 3219 GATGTCTGGTACCGTTACAAATTATCAGAGTAGTAAACTTGATATATGAG 3278
 Db 105 GATGTCTGGTACCGTTACAAATTATCAGAGTAGTAAACTTGATATATGAG 46

Qy 3279 GATATTAACATACATACTAGTATGATCGATGTCAGAAGT 3323
 Db 45 GATATTAACATACATACTAGTATGATCGATGTCAGAAGT 1

RESULT 10

US-09-439-313-162/C ; Sequence 162, Application US/09439313
 Patent No. 6329505 ;
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun ;
 ATTORNEY/AGENT INFORMATION: Dillon, Davin C. ;
 CURRENT APPLICATION NUMBER: 210121.427C9 ;
 CURRENT FILING DATE: 1999-11-12 ;
 NUMBER OF SEQ ID NOS: 575 ;
 SOFTWARE: FastSD for Windows Version 3.0 ;
 SEQ ID NO: 162 ;
 LENGTH: 177 ;
 TYPE: DNA ;
 ORGANISM: Homo sapien

US-09-439-313-162

Query Match Score 165; DB 4; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.2e-36;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3159 TTATGTTACCAAGACTGGTTATGCCAAGTTATCACCAGCTATGCTATGACTG 3218
 Db 165 TTATGTTACCAAGACTGGTTATGCCAAGTTATCACCAGCTATGCTATGACTG 106

Qy 3219 GATGTCTGGTACCGTTACAAATTATCAGAGTAGTAAACTTGATATATGAG 3278
 Db 105 GATGTCTGGTACCGTTACAAATTATCAGAGTAGTAAACTTGATATATGAG 46

Qy 3279 GATATTAACATACATACTAGTATGATCGATGTCAGAAGT 3323
 Db 45 GATATTAACATACATACTAGTATGATCGATGTCAGAAGT 1

RESULT 11

US-09-552-616A-162/C ; Sequence 162, Application US/09352616A
 Patent No. 6385278 ;
 GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C. ;
 ATTORNEY/AGENT INFORMATION: Harlockker, Susan Louise ;
 CURRENT APPLICATION NUMBER: 210121.427C8 ;
 CURRENT FILING DATE: 1999-11-12 ;
 NUMBER OF SEQ ID NOS: 575 ;
 SOFTWARE: FastSD for Windows Version 3.0 ;
 SEQ ID NO: 162 ;
 LENGTH: 177 ;
 TYPE: nucleic acid ;
 STRANDEDNESS: single ;
 TOPOLOGY: linear ;
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-030-607-162

Query Match Score 165; DB 3; Length 177;
 Best Local Similarity 100.0%; Pred. No. 2.2e-36;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 162
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Homo sapien
; FILE REFERENCE: GENSET .050CP23
; CURRENT APPLICATION NUMBER: US/09/599, 360B
; CURRENT FILING DATE: 2000-06-21
; PRIORITY APPLICATION NUMBER: 60/113, 686
; PRIORITY FILING DATE: 1998-12-22
; PRIORITY APPLICATION NUMBER: 60/141, 032
; PRIORITY FILING DATE: 1999-06-25
; PRIORITY APPLICATION NUMBER: 09/469, 099
; PRIORITY FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO: 3
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 139..1389
; NAME/KEY: sig_peptide
; LOCATION: 139..198
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.00
; OTHER INFORMATION: seq HLLAGECYWWVLG/KV
; NAME/KEY: polya_signal
; LOCATION: 1854..1859
; NAME/KEY: polyA_site
; LOCATION: 1873..1888
; US-09-599-360B-38

Query Match 3159 TTTATGATCAGACTGGCTTATGCCAAGTATAATACCAAAAGCTGTATGACTG 3218
Best Local Similarity 100.0%; Pred. No. 2.2e-36; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0;

QY 3219 GATGTCGTTGTTACAAATTATCAGACTGAAACTGATAATATGAG 3278
Db 105 GATGTCGTTGTTACCGTGTACAGATAATCAGATAATATGAG 46
QY 3279 GATATTAAACTACACTAACTATATTGATCGATGATGAGAAGT 3323
Db 45 GATATTAAACTACACTAACTATCATTTGATCGATGATGAGAAGT 1

RESULT 12
US-09-32-149A-162/C
; Sequence 162, Application US/09232149A
; Patent No. 646561
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Michan, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121_427C6
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 162
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Homo sapien
; FILE REFERENCE: GENSET .050CP23
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 162
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Homo sapien
; FILE REFERENCE: GENSET .050CP23
; CURRENT APPLICATION NUMBER: US/09/599, 360B
; CURRENT FILING DATE: 2000-06-21
; PRIORITY APPLICATION NUMBER: 60/113, 686
; PRIORITY FILING DATE: 1998-12-22
; PRIORITY APPLICATION NUMBER: 60/141, 032
; PRIORITY FILING DATE: 1999-06-25
; PRIORITY APPLICATION NUMBER: 09/469, 099
; PRIORITY FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO: 3
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 211; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.00
; OTHER INFORMATION: seq HLLAGECYWWVLG/KV
; NAME/KEY: polya_signal
; LOCATION: 1854..1859
; NAME/KEY: polyA_site
; LOCATION: 1873..1888
; US-09-599-360B-38

Query Match 3159 TTTATGATCAGACTGGCTTATGCCAAGTATAATACCAAAAGCTGTATGACTG 3218
Best Local Similarity 100.0%; Pred. No. 1.5e-20; Indels 1; Gaps 1;
Matches 211; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
Query Match 3219 GATGTCGTTGTTACAAATTATCAGACTGAAACTGATAATATGAG 3278
Best Local Similarity 58.4%; Pred. No. 1.5e-20; Indels 1; Gaps 1;
Matches 211; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
Query Match 3279 GATATTAAACTACACTAACTATATTGATCGATGATGAGAAGT 3323
Best Local Similarity 58.4%; Pred. No. 1.5e-20; Indels 1; Gaps 1;
Matches 211; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
Query Match 45 GATATTAAACTACACTAACTATCATTTGATCGATGATGAGAAGT 1
Best Local Similarity 58.4%; Pred. No. 1.5e-20; Indels 1; Gaps 1;
Matches 211; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

RESULT 14
US-08-980-571-64/C
; Sequence 64, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides

```

/ CITY: Seattle
 / STATE: Washington
 / COUNTRY: USA
 / ZIP: 98104
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC DOS/MS-DOS
 / SOFTWARE: PatentNet Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/990,571
 / FILING DATE: 11-DEC-1997
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Mai, David J.
 / REGISTRATION NUMBER: 31,392
 / REFERENCE/DOCKET NUMBER: 210121.426C2
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 622-4900
 / TELEFAX: (206) 682-6031
 / INFORMATION FOR SEQ ID NO: 64:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 285 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-990-571-64

Query Match 1.7%; Score 59.8; DB 3; Length 285;
 Best Local Similarity 65.2%; Pred. No. 7e-07; Indels 0; Gaps 0;
 Matches 88; Conservative 0; Mismatches 47;

QY 405 ATCCATACACCAGGACCATCACATCAGACGACGATTAGACGATGAG 464
 Db 192 AACCGTTCCTAGGCCACCGCTTCACTAGGCCACAGTTCTAGGCCACG 133

QY 465 CGTCACTGAGCCTAGGACATCACTAGAACGAGCACTGACCATGATCAC 524
 Db 132 CTTCATGGCCACAGCTTCACTAGGCCACCGCTTCACTAGGCCACGATTAC 73

QY 525 TCTAACATAATCAT 539
 Db 72 TAGCCCCACCAAGCTT 58

RESULT 15

US-09-528-784A-64/C
 / Sequence 64, Application US/09528784A
 / GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; TITLE OF INVENTION: AND TREATMENT OF B. MICOTI INFECTION
 ; FILE REFERENCE: 210121.4264
 ; CURRENT APPLICATION NUMBER: US/09/528,784A
 ; CURRENT FILING DATE: 2000-03-17
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 64
 ; LENGTH: 285
 ; TYPE: DNA
 ; ORGANISM: Babesia microti
 US-09-528-784A-64

Query Match 1.7%; Score 59.8; DB 4; Length 285;
 Best Local Similarity 65.2%; Pred. No. 7e-07; Indels 0; Gaps 0;
 Matches 88; Conservative 0; Mismatches 47;

QY 405 ATCCATACACCAGGACCATCACATCAGACGACGATTAGACGATGAG 464

Result No.	Score	Query Match	Length	DB ID	Description	\$	
1	3335.6	96.4	3586	14	US-10-176-847-51	Sequence 51, Appl	
2	3335.6	96.4	3537	14	US-10-198-846-10007	Sequence 10007, A	
3	2716	78.5	274	14	US-10-171-581-170	Sequence 170, App	
4	2716	78.5	2744	14	US-10-177-293-263	Sequence 263, App	
5	1141.4	33.0	1193	10	US-09-925-300-591	Sequence 591, App	
6	900.4	26.0	1449	14	US-10-198-846-10321	Sequence 10321, A	
7	694.2	20.1	1021	14	US-10-198-846-1805	Sequence 13805, A	
8	578.4	16.7	606	14	US-10-198-846-8190	Sequence 8490, App	
9	578.4	16.7	1598	14	US-10-198-846-11215	Sequence 11215, A	
10	404.8	11.7	483	10	US-09-867-701-2021	Sequence 2021, Ap	
c	11	390.8	11.3	395	9	US-09-778-320-94	Sequence 94, Appl
c	12	390.8	11.3	395	9	US-09-910-689-94	Sequence 94, Appl
c	13	390.8	11.3	395	13	US-10-010-742-94	Sequence 94, Appl
c	14	389.6	11.3	504	11	US-09-918-846-2272	Sequence 2222, A
c	15	360	10.4	385	9	US-09-827-669-78	Sequence 78, Appl
c	16	360	10.4	385	12	US-10-236-006-78	Sequence 78, Appl

QY	240	AAATTAGTCGGAAATGGGAATTCTGGGATTATGTTGACTTGGCAATTTCACGGCGA	299	1320	GCAATGGAAATGAAAGGACCACTTTCAGTCATCTGCTTCTCAAACATAGAGAA	1379	
Db	365	AAAATTAGTCGGAAATGGGAATTCTGGCAATTTCACGGCGA	424	1427	GCATGGAAATAAAGGACCACTTTCAGTCATCTGCTTCTCAAACATAGAGAA	1486	
QY	300	TATCATTACACAGTTTCTACGCTATGGAAATAATCTTGTCACTTGAAGG	359	1380	AGTGCATTATTGATTCAGTCAGCTGGGAAGGGTCAACAGCTTAGAGGCCCTGATTTCAG	1439	
Db	425	TATCATTACACAGTTTCTACGCTATGGAAATAATCTTGTCACTTGAAGG	484	1487	AGTGCATTATTGATTCAGTCAGCTGGGAAGGGTCAACAGCTTAGAGGCCCTGATTTCAG	1546	
QY	360	TTCGAAATAATCTCAAAATAGCATAGTAAAGAATCCATAGACAT	419	1440	TTTCUTTGATGACAGTCCTCAGTCATCTGCTTCTCAAACATTTAAGAGAAAGAT	1499	
Db	485	TTCGAAATAATCTCAAAATAGCATAGTAAAGAATCCATAGACAT	544	1547	TTTCUTTGATGACATCTCCACATTTGATCAACACATTAAAGAGAAAGAT	1606	
QY	420	GACACGACCATCATCACGCCAGGACATCACTGACCATGCGTCACGACAT	479	1500	CAGAGAACCTGAAATAATGATGATGATGGAGATAAGAGACCTGCTCAAGATGAA	1559	
Db	545	GACACGACCATCACGCCAGGACATCACTGACCATGCGTCACGACAT	604	1607	CAGAGAACCTGAAATAATGATGATGATGGAGATAAGAGACCTGCTCAAGATGAA	1666	
QY	480	GAGGATCACTCAAGACAGCATCACTCTGACCATGATCATCACTCACCATAATCAT	539	1560	TCTCAACTTCACAAATAAGGAGAAAGTAGATCAGATGACTGAACTGAGGTTATTA	1619	
Db	605	GAGGATCACTCAAGACAGCATCACTCTGACCATGATCATCACTCACCATAATCAT	650	1667	TCTCAACTTCACAAATAAGGAGAAATAATGATCAGATGACTGAACTGAGGCTTATTA	1726	
QY	540	GCTCTCTCTGTAAATAATGCCAAACCTTTCGCCACACATGACTCGATGTTA	539	1620	CGAGCAGACTCACAGACGCCCTCCACATTCAGTCATCACAGACAGTCAGCTGCAGTCAGTGGAAAGA	1679	
Db	651	---CTCTCTGTAAATAATGCCAAACCTTTCGCCACACATGACTCGATGTTA	706	1727	CGAGCAGACTCACAGACGCCCTCCACATTCAGTCATCACAGACAGTCAGCTGCAGTCAGTGGAAAGA	1786	
QY	600	GGTAAGATCCPAGAACACGCCAGGAAAGGCTCACCGACAGAACATGCCAGTGT	659	1680	GAAGAGCTCATGATGAGTCATGTCATCACAGGAAGTCAACAGAACTTACCCAGA	1739	
Db	707	GGTAAGATCCPAGAACACGCCAGGAAAGGCTCACCGACAGAACATGCCAGTGT	766	1787	GAAGAGCTCATGATGAGTCATGTCATCACAGGAAGTCAACAGAACTTACCCAGA	1846	
QY	660	AGAGGAATGTCAGGACAGCTGTAGTCCTAGTAGTGTACCTAACGTGTAAACACT	719	1740	GGGCCAGAAATAATGCCATTACATTCAGCAAGCTACACTGGCCCATGAGCTC	1799	
Db	767	AGAGGAATGTCAGGACAGCTGTAGTCCTAGTAGTGTACCTAACGTGTAAACACT	826	1847	GGGTECAGAAATAATGCCATTACATTCAGCAAGCTACACTGGCCCATGAGCTC	1906	
QY	720	GTCTCTGAGGACTACTTCTAGAGCAATAAGACCTCAAGACCTGGAAACCTTC	779	1800	ATTACACACCATGACTACCATGACTACCATGATGACTACCATGATGAACTAACCAACCAT	1859	
Db	827	GTCTCTGAGGACTACTTCTAGAGCAATAAGACCTCAAGACCTGGAAACCTTC	886	1907	ATTCACACCATGACTACCATGACTACCATGATGACTACCATGATGAACTAACCAACCAT	1966	
QY	780	CCCAAGAGTGTAGCAGCTCACROACCACTGTACACATAAAGACGCCGTGACCG	839	1860	CCTCACAGTCAGCCAGCCTGCGCTACTCTCGGGAGGCTGAAAGTGCCTGCCTGC	1919	
Db	887	CCCAAGAGTGTAGCAGCTCACROACCACTGTACACATAAAGACGCCGTGACCG	946	1957	CCTCAAGTCACGCCAGCCTGCGCTACTCTCGGGAGGCTGAAAGTGCCTGCCTGC	2026	
QY	840	CTGGCTGTAGAAACAAATGACTCTGTGTAGTGGCCCGAAAGGTTATGATTC	899	1920	TTGGCCGTGATGGTGTAAATGGGTGATGCCCTGCACAAATTCTGGGATGCTTACATGAA	1979	
Db	947	CTGGCTGTAGAAACAAATGACTCTGTGTAGTGGCCCGAAAGGTTATGATTC	1006	2027	TTGGCCGTGATGGTGTAAATGGGTGATGCCCTGCACAAATTCTGGGATGCTTACATGAA	2086	
QY	900	AGAACACAATAAACTTCAGGAGCTCAAGTCATGACTGATGACTGATC	959	1980	GTTGCTGCTTCTGAGGTTACAGTCAGTCATGTTAGTACTCTGTTCTGCTCT	2039	
Db	1007	AGAACACAATAAACTTCAGGAGCTCAAGTCATGACTGATGACTGATC	1066	2087	GTCGCTGCTTCTGAGGTTACAGTCAGTCATGTTAGTACTCTGTTCTGTTCTG	2146	
QY	960	GGCATGGGCAATGGTTCCCTGATGCAAGGTTCAACTATCTGTCAAGCCTC	1019	2040	CATGAGTTGCCTATGATGTTAGTGTACTCTGCTGTTCTACTAAAGGCTGCACTGACGCT	2099	
Db	1067	GGCATGGGCAATGGTTCCCTGATGCAAGGTTCAACTATCTGTCAAGCCTC	1126	2147	CATGAGTTGCCTCAGTCAGTAACTGTTAGTGTACTCTGCTGTTCTACTAAAGGCTGCACTGACGCT	2206	
QY	1020	ATCACACCAATAATGATGATGATGCTGTTGATGCTGAAAGGCTGAAATC	1079	2160	GAAATTTCATGGTCATGTTGAGGATTTGGAAATGTTCTATGGGATTTGCTACTGCT	2219	
Db	1127	ATCACACCAATAATGATGATGCTGTTGATGCTGAAAGGCTGAAATC	1186	2247	GGAAATTTCATGGTCATGTTGAGGATTTGGAAATGTTCTATGGGATTTGCTACTGCT	2326	
QY	1080	CCTCAAAACCTCATACAAATGACTGCTGGGTTTAACTGCTTCTCAATGAACT	1139	2220	GGCTTATTGATGTTGCTGCTGGCTCTGCTGACATGTTGATGTTGATGCTGCT	2279	
Db	1187	CCTCAAAACCTCATACAAATGACTGCTGGGTTTAACTGCTTCTCAATGAACT	1246	2327	GGCTTATTGATGTTGCTGCTGGCTCTGCTGACATGTTGATGCTGCT	2386	
QY	1140	ATCACTTTCGTCGTTCTGCTGGCTCTGCTGCTGGCTCTGCTGCTGGCTCT	1199	QY	2240	GGTTGGAAATTATGTTACTTCAATTGCTAAATGTTCAAGAATAATGTTCTGCT	2399
Db	1247	ATCACTTTCGTCGTTCTGCTGGCTCTGCTGCTGGCTCTGCTGCTGGCTCT	1306	2387	AGTGCACCTGGATGCTGGCTCTGCTGCTGGCTCTGCTGCTGGCTCTGCT	2446	
QY	1200	AAATTTCCTGCTGTTCTGCTGGCTCTGCTGCTGGCTCTGCTGCTGGCTCT	1259	2447	GGTTGGAAATTATGTTACTTCAATTGCTAAATGTTCAAGAATAATGTTCTG	2504	
Db	1307	AAATTTCCTGCTGTTCTGCTGGCTCTGCTGCTGGCTCTGCTGCTGGCTCT	1366	2400	TTCTAGTTAGGTTAAATGCTAGTACTCTTAAAGTGTCAAGTGTCAAGTGTCA	2459	
QY	1260	TTACACCTCTTCACATTCACATTCACATTCACATTCACATTCACATTCAC	1319	QY			
Db	1367	TTACACCTCTTCACATTCACATTCACATTCACATTCACATTCACATTCAC	1426				

Db |||||||TTCTAGTAACTTTAATCTAAGTACGCTTAAAGTGTCA 2554
 QY : Sequence 10007; Application US/10198846
 Public No. US2003009977A1
 GENERAL INFORMATION:
 / APPLICANT: Lillie, James
 / APPLICANT: Xu, Yongyao
 / APPLICANT: Wang, Youzhen
 / APPLICANT: Steinmann, Kathleen
 / TITLE OF INVENTION: NOVEL KITS, COMPOSITIONS, KITS, AND METHODS
 / FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 / THERAPY OF BREAST CANCER
 CURRENT APPLICATION NUMBER: US/10/198, 846
 CURRENT FILING DATE: 2002-07-18
 / PRIORITY NUMBER: 60/306, 220
 / PRIORITY FILING DATE: 2001-07-18
 NUMBER OF SEQ ID NOS: 14084
 SOFTWARE: PastSeq for Windows Version 4.0
 SEQ ID NO 10007
 LENGTH: 3537
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: 1, 2, 3533, 3534, 3535, 3536, 3537
 / OTHER INFORMATION: n = A, T, C or G

Db |||||||TTATCTATCTGGATAAAATCTGTATGTCATTGCAATTACCGGATTAAGTAAAGCTTAAAGTGTCA 2634
 QY : US/10/198, 846
 Db |||||||TTATCTATCTGGATAAAATCTGTATGTCATTGCAATTACCGGATTAAGTGTCA 2639
 QY : US/10/198, 846
 Db |||||||TTATCTATCTGGATAAAATCTGTATGTCATTGCAATTACCGGATTAAGTGTCA 2744
 QY : US/10/198, 846
 Db |||||||TTATCTATCTGGATAAAATCTGTATGTCATTGCAATTACCGGATTAAGTGTCA 2699
 QY : US/10/198, 846
 Db |||||||TTATCTATCTGGATAAAATCTGTATGTCATTGCAATTACCGGATTAAGTGTCA 2804
 QY : US/10/198, 846
 Db |||||||TTATCTAGAAGTAACTAACAGCTTAACTCTTACTGATTAGGCTCTGAAACCTG 2759
 QY : US/10/198, 846
 Db |||||||TTCTCAGAAGTAACTAACAGCTTAACTCTTACTGATTAGGCTCTGAAACCTG 2864
 QY : US/10/198, 846
 Db |||||||TTCTTGGAAATAGGAATGNGCATGAAAGCTTATACTGAATT 2819
 QY : US/10/198, 846
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 Db |||||||TTAAATAATTTAATGAAATAACACTGACCAAGAAATTGGAATTCAAAT 3119
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 Db |||||||TTAAATAATTTAATGAAATAACACTGACCAAGAAATTGGAATTCAAAT 3224
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 Db |||||||TTCTGGGGTTATACCAGATGACATGTTGAGTACAGACTGG 3179
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 Db |||||||TTCTGGGGTTATACCAGATGACATGTTGAGTACAGACTGG 3284
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 Db |||||||TTATGCCAAGTTATCAGTAAACTTGATATAAGGATAACTCACTAGT 3299
 QY : US/10/198, 846
 Db |||||||TTATGCCAAGTTATCAGTAAACTTGATATAAGGATAACTCACTAGT 3404
 QY : US/10/198, 846
 Db |||||||ATCATTGATTGATGAAAGTGTGATGTTGATCTCAGTCAGTGTCTGTT 3359
 QY : US/10/198, 846
 Db |||||||ATCATTGATTGATGAAAGTGTGATGTTGATCTCAGTCAGTGTCTGTT 3464
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 Db |||||||TGAGAAATGCTCTTATAGGCTGACTGACATATAAGCTGCTGCGATCT 3419
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 QY : US/10/198, 846
 Db |||||||AGATTTCTTATACATAATACTCTTATACAGCTTG 602
 QY : US/10/198, 846
 Db |||||||GCTTCGGTTAAATAAGCAGCCAGCTGACTGATGATGATGATGATG 584
 QY : US/10/198, 846

QY	2823	CAAGAAATAACGGAGAAAAGACAATGTGACATTGGGAGCCATAGATCTTAA	2882	QY	1	CTCGGCCGAATTCCGCACAGCAGCCGGGTTCGGCTGGTAGATTTCTCGAAGACA	60
Db	2805	CAAGAAATAACGGAGAAAAGACAATGTGACATTGGGAGCCATAGATCTTAA	2864	Db	1	CTCGGCCGAATTCCGCAGAGCAGCCGGGTTCGGCTGGTAGATTTCTCGAAGACA	60
QY	2883	AAATCACAAATTGTTGTAATTAGGGGAGAAATTAGATAATTGTGACATTGGGAGCC	2942	QY	61	CCAGTGGCCCGTGTGAAACCAAAACTCGGCCGTCGGGGGAGAACCGAGCC	120
Db	2865	AAATCACAAATTGTTGTAATTAGGGGAGAAATTAGATAATTGTGACATTGGGAGCC	2924	Db	61	CCAGTGGCCCGTGTGAAACCAAACTCGGCCGTCGGGGGAGAACCGAGCC	120
QY	2943	GAATAGTATAGAGTCAATTATTAACATTGGGAGATTTCGGTAAACAGT	3002	QY	121	GCGGAGGAGGGCAATTGGGAGGAGTATCTGAACTCTGACCTTGCCC	180
Db	2925	GAATAGTATAGAGTCAATTATTAACGGGAGAAATTAGATAATTTCGGTAAACAGT	2984	Db	121	GCGGAGGAGGGCAATTGGCAGGAGTATCTGAACTCTGACCTTGCCC	180
QY	3003	AGTAGGACAC-TCTGATTAACATAATT-ACTGTACATTAACCTGATATACGAAATC	3059	QY	181	TCTCTGTCACAAATCCCCCTCATGAACTTAAAGCAGCTGCTTCCCCAGACCACTGAGA	240
Db	2985	AGTAGGACACTTTCAATACATAATTACTGTACATTAACCTGATATACGAAATC	3044	Db	181	TCTCTGTCACAAATCCCCCTCAAGAAATTCCCGACAGCAGCTGCTTCCCCAGACCACTGAGA	240
QY	3060	TAATAATATTAATGAAATTCAAGCAATAATA-CACTTGACCAAGAAATTGGAAATTCAA	3118	QY	241	AATTATGTCGCAATTGGGAAATCTGGCATTAAATGTGACCTGGCAATTTCACGGCAAT	300
Db	3045	TAATAATATTAATGAAATTCAAGCAATAATACTGACCAAGAAATTGGAAATTCAA	3104	Db	241	AATTATGTCGCAATTGGGAAATCTGGCATTAAATGTGACCTGGCAATTTCACGGCAAT	300
QY	3119	TGTCTGTCGGGTATATACCAAGTACAGTAG-TTATATGATCACAGACTG	3177	QY	301	ATCATACAAACAGCTTTCTACGGCATATGGAAATAATTCTTGTGAGTTGAGGT	360
Db	3105	TGTCTGTCGGGTATATACCAAGTACAGTAG-TTATATGATCACAGACTG	3163	Db	301	ATCATACAAACAGCTTTCTACGGCATATGGAAATAATTCTTGTGAGTTGAGGT	360
QY	3178	GTTATTGGCAAGTATATACTACACAAAGCTGTATGCTGTTACCTGGT	3237	QY	361	TCAAAATTACTCAAAATAAGCATAGATAAGATAAAAGATCCATATACCATG	420
Db	3164	GTTATTGGCAAGTATATACTACACAAAGCTGTATGCTGTTACCTGGT	3223	Db	361	TCAAAATTACTCAAAATAAGCATAGATAAGATAAAAGATCCATATACCATG	420
QY	3238	TTACAAAATTATCAGTACAGTAACACTTGAGTATAGGATAATAACTACACTAA	3297	QY	421	ACCAGGACCATCACTAGACCAAGGACATCACTCGACGACCATGAGCTGCACTGAGACCATG	480
Db	3224	TTACAAAATTATCAGTACAGTAACACTTGAGTATAGGATAATAACTACACTAA	3283	Db	421	ACCAGGACCATCACTAGACCAAGGACATCACTCGACGACCATGAGCTGCACTGAGACCATG	480
QY	3298	GTTATCTTGGTATACCAAGTACAGTAGTACAGTAGTACAGTAGTACAT	3357	QY	481	AGCTCACTCGACCCAGCAGCATCTGACCATGATCATCTACCTCACTCTACCTAATCTG	540
Db	3284	GTTATCTTGGTATACCAAGTACAGTAGTACAGTAGTACAGTAGTACAT	3343	Db	481	AGCTCACTCGACCCAGCAGCATCTGACCATGATCATCTACCTCACTCTACCTAATCTG	522
QY	3358	TGTGACCAATTGTC-TTATACTAGTACAGTACAGTACAGTACAGTACAT	3416	QY	541	CTGCTCTGGTAAATAAGCAGAAAGCTTGTGCCAGCCTGACCTAGTACGTAGTCAG	600
Db	3344	TGTGACCAATTGTC-TTATACTAGTACAGTACAGTACAGTACAGTACAT	3403	Db	523	CTGCTCTGGTAAATAAGCAGAAAGCTTGTGCCAGCCTGACCTAGTACGTAGTCAG	582
QY	3417	TCTAGATGTTCTTTTACACAAATTCCCTTATATCAGC	3458	QY	601	GTAAGATCCTAGAAACAGCCAGGGAAAGGCTCACCCGACCAAGATGCCAGTGTAGTCAG	660
Db	3404	TCTAGATGTTCTTTTACACAAATTCCCTTATATCAGC	3445	Db	583	GTAAGATCCTAGAAACAGCCAGGGAAAGGCTCACCCGACCAAGATGCCAGTGTAGTCAG	642
QY	RESULT 3						
US-10-171-581-170	Sequence 170, Application US/10171581						
; GENERAL INFORMATION:	; Publication No. US20030104426A1						
; APPLICANT: Dai, Hongrye							
; APPLICANT: Linsley, Peter							
; APPLICANT: Mao, Mao							
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia							
; FILE REFERENCE: 9301:157-999							
; CURRENT APPLICATION NUMBER: US/10/171,581							
; CURRENT FILING DATE: 2002-06-14							
; PRIOR FILING DATE: 2001-06-18							
; SEQ ID NO: 170							
; LENGTH: 2744							
; ORGANISM: Homo sapiens							
; PUBLICATION INFORMATION:							
; DATABASE ACCESSION NUMBER: U41060							
; DATABASE ENTRY DATE: 2001-06-18							
US-10-171-581-170							
Query Match	78.5%	Score	2716;	DB	14;	Length	2744;
Best Local Similarity	90.3%	Pred. No.	0;	Indels	18;	Gaps	1;
Mismatches	2744;	Conservative	0;				

Page 8

	RESULT	5
QY	1861	CTTACAGTCACGCCCTACTCTGGGGAGCTGAAAGATGCCGTGCCACTT
	1843	CTTACACTCAAGCCAGCCTATACTGGGAGCTGAAAGATGCCGTGCCACTT
QY	1921	TGCCCTGGATGGTATAATGGGATAGGGCATGGCTGCCAACATTTCAGCGATGGCTAGAACATT
	1903	TGCCCTGGATGGTATAATGGGATAGGGCATGGCTGCCAACATTTCAGCGATGGCTAGAACATT
QY	1981	GTCCTGGTTTAAGGCCTATCAAGTGGTTAAGTACTCTGTCGTCGTCGTC
	1963	GTCCTGGTTTAAGGCCTATCAAGTGGTTAAGTACTCTGTCGTCGTCGTC
QY	2041	ATSGAGTGCCTAGAATAGTGACTCTGGTCTACTAAAGGCTGGCATGACCGTAA
	2023	ATAGTGCCTAGAATAGTGACTCTGGTCTACTAAAGGCTGGCATGACCGTAA
QY	2101	AGAGGCTGCCCTTATATGCCATTTCTGGCATATCTGGATGGCACAG
	2083	AGCAGGTGGCTCTTATATGCCATTTCTGGCATATCTGGATGGCACAG
QY	2161	GAATTTCATGGCATATGCCATATGCCAAATGGTTATGGGATATTCGCAATTACTGTC
	2143	GAATTTCATGGCATATGCCATATGCCAAATGGTTATGGGATATTCGCAATTACTGTC
QY	2221	GCTTATTCATCTGGTGTCTGGTATATGGTACCTAAATGCTGCCACATGCTGA
	2203	GCTTATTCATCTGGTGTCTGGTATATGGTACCTAAATGCTGCCACATGCTGA
QY	2281	GTGACCATGGATGATGACGCCCTGGGSTATTCCTTTACAGATGCTGGGATGCTTTGG
	2263	GTGACCATGGATGATGACGCCCTGGGATTTACAGATGCTGGGATGCTTTGG
QY	2341	GTTTGGAAATTGTTACTATTCATATTGCCATATACTGTTTGTGATAATT
	2323	GTTTGGAAATTGTTACTATTCATATTGCCATATACTGTTTGTGATAATT
QY	2401	TCTAGTAAGTTAAATGCTAGTAGCTAAAGATGCTATGGTCAATGGTTCTAGTGCTAT
	2383	TCTAGTAAGTTAAATGCTAGTAGCTAAAGATGCTAGCTAAATGGTCAATGGTCTAT
QY	2461	AGGGAGATGAGTTGTTGTTGACTATGCAAGCTTAAAGGTGAGGTTTGKATT
	2443	AGGGAGATGAGTTGTTGACTATGCAAGCTTAAAGGTGAGGTTTGKATT
QY	2521	TCTATGAAATGCTGCTGTTACAAAGTCAGTAAAGGTGCTTTATATTAACT
	2503	TCTATGAAATGCTGCTGTTACAAAGTCAGTAAAGGTGCTTTATATTAACT
QY	2581	TATTCTATCTGGATGATAAAATGTTGTCGCAATCACGGTAACTTATGTTAATGCT
	2563	TATTCTATCTGGATGATAAAATGTTGTCGCAATCACGGTAACTTATGTTAATGCT
QY	2641	TAACAGAGATTTGGCATGACATGGTCTGTTACGGTAACTTACGGTAACTTAACT
	2623	TAACAGAGATTTGGCATGACATGGTCTGTTACGGTAACTTACGGTAACTTAACT
QY	2701	TTTCAGAACTTACACGTTATCCATATGGGATTAGGCTCTGAAAGACTGCTG
	2683	TTTCAGAACTTACACGTTATCCPATAGGATTAGGCTCTGAAAGACTGCTG
QY	2761	TG 2762
	2743	TG 2744
Db		

RESULT 5
 US-09-925-300-591
 Sequence 591, Application US/09925300
 ; Parent No. US2002015168A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Rubin

Db	661	GAGGACACTTTCAGTCATCTGCTCTCAAAATAAGAGAGTGCCATTGATI	720
QY	1396	CCAGTGGAAAGGTAAACGCTTAGGGCTGTATTCTGTGAACATG	1455
Db	721	CCAGTGGAAAGGTAAACGCTTAGGGCTGTATTCTGTGAACATG	780
QY	1456	TCCCATGGATCAACATTAAAGATAAGAAAAGAACGAGAACGAAA	1515

781 TCCATCATTGTCACATTTAAAGATAAAGAAAAGATCAGAAAACCTGAA 840
 Db QY 1516 ATGATGATGATGGAGATAAGAGCACTTGTCCAAGTGAATGTAACCTTCACAA 1575
 Db QY 841 ATGATGATGATGGAGATAAGAGCACTTGTCCAAGTGAATGTAACCTTCACAA 900
 Db QY 1576 ATGAGGAAAAGTAAATGACAGATGCAACTGAAAGCTTATTCAGASAGACTCAAG 1635
 Db QY 901 ATGAGGAAAAGTAAATGACAGATGCAACTGAAAGCTTATTCAGASAGACTCAAG 960
 Db QY 1636 AGCCCTCCOACTTGTGATTCAGCAGCTGCAGTCTGGAGAGAGAGGTCATGATAG 1695
 Db QY 961 AGCCCTCCOACTTGTGATTCAGCAGCTGCAGTCTGGAGAGAGGTCATGATAG 1020
 Db QY 1696 CTARGCTCATCCACAGAAGCTCAATGATTAATGATTAATGATTAATGATTAAT 1755
 Db QY 1021 CTARGCTCATCCACAGAAGCTCAATGATTAATGATTAATGATTAATGATTAAT 1080
 Db QY 1756 GCCATTCACATTCACGGCATCACGCCAGTCAGCAGTCATTCACCCATCATG 1815
 Db QY 1081 GCCATTCACATTCACGGCATCACACTCGGCCAGTCAGCAGTCATTCACCCATCATG 1140
 QY 1816 ACT 1818
 Db QY 1141 ACT 1143
 Db QY 1144 ACT 1143

RESULT 6
 US-10-198-846-10321
 ; Sequence 10321, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yonyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198, 846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306, 220
 ; PRIOR FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 10321
 ; LENGTH: 1449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1447, 1448, 1449
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-10321

Query Match 26.0%; Score 900.4; DB 14; Length 1449;
 Best Local Similarity 96.4%; Pred. No. 9; ge-219;
 Matches 985; Conservative 0; Mismatches 31; Indels 6; Gaps 6;

QY 1104 ATAGCTGGATGTTGCTGGTTTATAGCATTCCATCATCAGTTTCGTCGCGGG 1163
 Db 199 ACAGCTGGTTGGTGGTTATAGCATTCCATCATCAGTTTCGTCGCGGG 258
 ; Sequence 13805, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER

QY 1164 GTTATCTTGTGCTCTCATGATGGGTGTTTCAATTCTCGTGAATTCCTGTCGTG 1223
 Db 259 GTTATCTTGTGCTCTCATGATGGGTGTTTCAATTCTCGTGAATTCCTGTCGTG 318
 ; Sequence 13806, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER

QY 1224 GCAGTGCCGTTGGACTTGTGATGCTTACACTTCCTACACATTCTCAT 1283
 Db 319 GCACTGCCGTTGGACTTGTGATGCTTACACTTCCTACACATTCTCAT 378

	QY	2665	GTCGTGATGGTTTCAAGAAAATGCTTTAATGCTTTCAAGAACTAACAGTTATT 274
430 GATCGACTAAGGCTATTACAGCAGACTCACAGACCCCTGCCCTTGATCTCG 489	Db	1096	GTCGTGATGGTTTCAAGAAAATGCTTTCAAGAACTAACAGTTATT 1155
1659 CAGCCCTGAGTCCTGGAAAGAGGTATGCTATGGTATCCAGGAAGTC 1718	QY	2725	CCTATACTGGATTCTGGTCAAGCTGGCTCGTTAGGAAATAAGAATGTCGATG 2784
490 CGCCCTGAGTCCTGGAAAGAGGTATGCTATGGTATCCAGGAAGTC 549	Db	1156	CCATATGGATTCTGGCTCGTTAGGAAATGCTTTCAAGAACTAACAGTTATT 1214
1719 TACAATGAAATATGACCCAGAGGGTGCAGATAATGCTACATTTCCACCA 1774	QY	2785	AACCTTAATACACAGAAAGCTTATCTGAAAGGAAATTAGCAAGAAATAAGGAAAGA 2844
550 TACAATGAAATATGACCCAGANGTCGAGATAATGCTACATTTCCACCA 605	Db	1215	AACCTTAATACACAGAAAGCTTATCTGAAAGAAATAAGGAAAGA 1274
	QY	2845	GAGAACTGAAATTGGGGAGCATGTTAAATACAAATTTGGTAA 2904
	Db	1275	GAGAACTGAA-TGGGGGGATAGA-TCTTAAATACAAATTCGTT-GTAA 1330
	QY	2905	TAGAGGGGAAATTAATTGAAATAGCTGAAAGGAAATTAGTATAGCTCATACTA 3023
	Db	1331	TGAGGGGAAATTAACGGCAATTAGCTGAACTGTCGAGTCAT 1390
	QY	2964	ATTAAGATTTGTCAGGATTATTCGGTAAACCTGAGCTCTCATACTA 3023
	Db	1391	CTGACACCTCTCGTC-GGATTATTCGGTAAACGTGTCGCCCTTCATCAATT 1449
	QY	3024	ATTAGTGTCACATT 3037
	Db	1450	TGGTGTCTTACTT 1463
	QY	RESULT 10	
	Db	US-09-867-701-2021	
	QY	; Sequence 2021, Application US/09867-701	
	Db	; Patent No. US20020132237A1	
	QY	; GENERAL INFORMATION:	
	Db	; APPLICANT: Aglata, Paul A.	
	QY	; ATTORNEY: Jones, Robert	
	Db	; APPLICANT: Harlocker, Susan L.	
	QY	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
	Db	; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND	
	QY	; TITLE OF INVENTION: THERAPY OF BREAST CANCER	
	Db	; FILE REFERENCE: MRI-049	
	QY	; CURRENT APPLICATION NUMBER: US/10/198,846	
	Db	; CURRENT FILING DATE: 2003-07-18	
	QY	; NUMBER OF SEQ ID NOS: 14084	
	Db	; LENGTH: 1598	
	QY	; SOFTWARE: FastSEQ for Windows Version 4.0	
	Db	; SEQ ID NO: 11215	
	QY	; OTHER INFORMATION: n = A,T,C or G	
	Db	; LENGTH: 1598	
	QY	Query Match 16.7%; Score 578.4; DB 14; Length 1598;	
	Db	Best Local Similarity 91.3%; Pred. No. 1.5e-136; Mismatches 0; Indels 13; Gaps 10;	
	QY	2245 TGTATGGTACCTGAAATGCTGACATGATGTCAGTGTGCAATGATGCTGG 2304	
	Db	682 TTTTAAGGACTCTTACAGATGCTGGATGCTTTCGGTTGGATTATGTCAGT 741	
	QY	2305 GGTATTTCCTTACAGATGCTGGATGCTTTCGGTTGGATTATGTCAGT 2364	
	Db	742 GTGATTCCTTACAGATGCTGGATGCTTACAGTTCAGTGTGCAATGCTGG 799	
	QY	2365 CCTATTTGACATAAACCTGTTCTCATATACTCTAGTTTAAATGCTGTA 2424	
	Db	800 CCATATTGACATAAAATGCTGGTTCTATAAATTCTAGTTAGTTAAATGCTGTA 859	
	QY	2425 GTAGCTAAAGTGTCTATAGTTCACTAGTTCACTAGGAGATGAGTTGTATGCTGTA 2484	
	Db	860 GTTGTCTTAAAGTGTCTAGGATCTAGGAGAGAG-TTGTATGCTGTA 918	
	QY	2485 CTATGCCGCTTAAAGTGTCTAGGATCTAGGAGAGAG-TTGTATGCTGTA 2544	
	Db	919 CTATGCCGCTTAAAGTGTCTAGGATCTAGTGTGTTAATGCTGTT 976	
	QY	2545 ACAGCTGCTTAAAGTGTCTATAGTTCACTAGTCTAGGAGATGAGTTGTATGCTGTA 2604	
	Db	977 ACAAGCTGCTTAAAGTGTCTATAGTTCACTAGTCTAGGAGATGAGTTGTATGCTGTA 1036	
	QY	2605 GTATGCTGAACTACCGTTATTCCAGTTATATGATGAACTAGGAGATGGCTGACAT 2664	
	Db	1037 GTATGCTGAACTACCGTTATTCCAGTTATATGATGAACTAGGAGATGG-ATGCT 1095	
	QY	2721 TATCCCTTAACTGCTGTTAGCTCTGAGAACTGCTGGTGTAGGATATAAGAATG 2780	
	Db	182 TATCCCTTAACTGCTGTTAGCTCTGAGAACTGCTGGTGTAGGATATAAGAATGATG 241	

2781 CATGAAAGCCTAAAATACCAAGAAAGCTTATACTGAATAAGGAGAA 2840
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2412 CTGAAAGCCTAAAATACCAAGAAAGCTTATACTGAATAAGGAGAA 301
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2841 AGAGAGAGATC-TGGAAATTGGGAGGCATAGATTCTTATACCAAAATTGT 2898
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 302 AGAGAGAGATCCTGGAGATTCGTTGAGGATAGATTCTAACAAATTGT 361
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2899 TCTAAATTCAGGGGAAATTAGATAGATAAGCCTAAAGGCGATTAGTAGGT 2957
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 362 TGTGAAATTTCAGGGGAAATTAGATAGATAAGCCTAAAGGCGATTAGTAGGT 421
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2958 ACATCATTAACATTGTCGAGGATTTCCTGGTAAAGCTGTGACCACTCT 3017
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 422 ACNTCTTAACTAACATTGCGGGATTATTCGGGTAAACGGTGGGGCCTTCG 481
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 3018 AT 3019
 QY |||||
 Db 482 AT 483
 QY |||||

RESULT 11
 US-09-778-3220-94/C
 Sequence 94, Application US/09778320
 ; Patient No. US2010034052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121_491C6
 ; CURRENT APPLICATION NUMBER: US/09/910,689
 ; CURRENT FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 94
 ; LENGTH: 395

Query Match 11.3%; Score 390; DB 9; Length 395;
 Best Local Similarity 99.2%; Prod. No. 3..e-89; Indels 0; Gaps 0;
 Matches 392; Conservative 0; Mismatches 3; Name/KEY: misc_feature
 ; LOCATION: (1)..(395)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-778-3220-94
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(395)
 ; OTHER INFORMATION: n = A,T,C or G

Query Match 11.3%; Score 390.8; DB 9; Length 395;
 Best Local Similarity 99.2%; Prod. No. 3..8e-89; Indels 0; Gaps 0;
 Matches 392; Conservative 0; Mismatches 3; Name/KEY: misc_feature
 ; LOCATION: (1)..(395)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-778-3220-94
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(395)
 ; OTHER INFORMATION: n = A,T,C or G

2563 ACGTTTATTTTAACTTAAAGTTCTCTGGAGATAAAATCTGTATGCAATTACCGG 2622
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 395 ACGTTTATTTTAACTTAAAGTTCTCTGGAGATAAAATCTGTATGCAATTACCGG 336
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2623 TAATCCAGTTTATTTATGATTAACAAAGAGATTTGGCATGATCTTGATGTTACCGG 2682
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 335 TAATCCAGTTTATTTATGATTAACAAAGAGATTTGGCATGATCTTGATGTTACCGG 2742
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2683 AAAATGTCCTTAACTGCTTAACTGAAACTACACAGTTATCTCTTACCGG 2742
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 275 AAAATGTCCTTAACTGCTTAACTGAAACTACACAGTTATCTCTTACCGG 2802
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 215 AGCTTATCTGATTTAGTAACTGCTGTGTTAGTAAAGATGCTTACCGG 2864
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2863 GGAGCCATGATGCTTAAATCACAATTTGTGTAATAGGGGAGAAATTAA
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 95 GGAGCCATGATGCTTAAATCACAATTTGTGTAATAGGGGAGAAATTAA
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2923 GAATTAAGTAAAGCCAAATTAGCCTTAACTGCTTAACTGCTTACCGG 2862
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 35 GAATTAAGTAAAGCCAAATTAGCCTTAACTGCTTAACTGCTTACCGG 1
 QY ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


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; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-642-034-1.rnpb

Query Match      10.4%; Score 360; DB 9; Length 385;
Best Local Similarity 98.2%; Pred. No. 2.7e-81;
Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
QY      TAGGTTATAGGGAAATGAGTTGTTGACTATGAGCGTTTAAGTTAGGGTT 2512
Db      TGGTCAATAGGAGA-GATTGTGTTGACTATGAGCGTTTAAGTTAGGGTT 58
QY      TGTGATTTTCTATGAAATATTCCTGTTACAAACGTTAACAGTTAACGTTTAT 2572
Db      59 TGTGATTTTGTATGAAATATGCTGTCGTGTTACAAAGCTTAAAGGTAACGTATTAT 118
QY      ATTAAAGTTATCTATCTGGAGATAAAACCTGTAATCACCCTTACCGAT 2632
Db      119 ATTAAAGTTATCTATCTGGAGATAAAACCTGTAATCACCCTTACCGAT 178
QY      TTAATATGTAACAGAGATTCGGTACATGGTCTGATTTTCAGGAAAAATGCT 2692
Db      179 TTAATATGTAACAGAGATTCGGTACATGGTCTGATTTTCAGGAAAAATGCT 238
QY      TTAATCTTTCAAGAACTAACAGTTACACGTTATCCATTACTGAAATTAGGTCTGAGA 2752
Db      239 TTAATGTTTCAGAACTAACAGTTACACGTTATCCATTACTGAAATTAGGTCTGAGA 298
QY      ACTGCTGGTTAGAAATAGATGGCATGAACCTPAAAATACCAAGAAAGCTTATAC 2812
Db      299 ACTGCTGGTTAGAAATAGATGGCATGAACCTPAAAATACCAAGAAAGCTTATAC 358
QY      2813 TGATTAAAGAAAGAAATAA 2834
Db      359 TGATTAAAGAAAGAAATAA 380

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Search completed: September 12, 2003, 22:12:41
 Job time : 804.001 secs

Page 1

GenCore version 5.1.6						
Copyright (c) 1993 - 2003 Compugen Ltd.						
I nucleic - nucleic search, using sw model						
run on:	September 12, 2003, 16:38:39 ;	Search time 126.286 Seconds				
	(without alignments)					
	7926.909 Million cell updates/sec					
title:	US-09-642-034-4					
perfect score:	2268					
Sequence:	1 atggcaggaaagtatctgt.....tgtttcgataaaatttctatg 2268					
scoring table:	IDENTITY_NUC					
Gapext:	Gapext 1.0					
searched:	569978 seqs, 220691566 residues					
total number of hits satisfying chosen parameters:	1139956					
minimum DB seq length:	0					
maximum DB seq length:	2000000000					
hit-processing:	Minimum Match 0%					
	Maximum Match 10%					
	Listing first 45 summaries					
database :						
	Issued Patents NA:*					
1:	/cgn2_6/podata/2/ina/54.COMB.seq;*					
2:	/cgn2_6/podata/2/ina/5B.COMB.seq;*					
3:	/cgn2_6/podata/2/ina/6A.COMB.seq;*					
4:	/cgn2_6/podata/2/ina/6B.COMB.seq;*					
5:	/cgn2_6/podata/2/ina/PCVUS.COMB.seq;*					
6:	/cgn2_6/podata/2/ina/backfile1.seq;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Length	DB ID	Description		
1	1263	55.7	1310	1 US-08-311-023-1		
2	1263	55.7	2404	1 US-08-311-023-3		
3	110.6	4.9	1888	4 US-09-599-360B-38		
4	59.8	2.6	285	3 US-08-590-571-64		
5	59.8	2.6	285	4 US-09-528-784A-04		
6	59.8	2.6	285	4 US-09-569-098A-64		
7	59.8	2.6	342	3 US-08-590-571-65		
8	59.8	2.6	342	4 US-09-528-784A-65		
9	59.8	2.6	342	4 US-09-569-098A-65		
10	59.8	2.6	351	3 US-08-590-571-60		
11	59.8	2.6	351	4 US-09-528-784A-60		
12	59.8	2.6	351	4 US-09-569-098A-60		
13	59.8	2.6	356	3 US-08-590-571-63		
14	59.8	2.6	356	4 US-09-528-784A-63		
15	59.8	2.6	356	4 US-09-569-098A-63		
16	59.8	2.6	358	3 US-08-590-571-58		
17	59.8	2.6	358	4 US-09-528-784A-58		
18	59.8	2.6	358	4 US-09-569-098A-58		
19	59.8	2.6	363	3 US-08-590-571-66		
20	59.8	2.6	363	3 US-08-590-571-67		
21	59.8	2.6	363	4 US-09-528-784A-66		
22	59.8	2.6	363	4 US-09-528-784A-67		
23	59.8	2.6	363	4 US-09-569-098A-66		
24	59.8	2.6	363	4 US-09-569-098A-67		
25	59.8	2.6	409	3 US-08-590-571-59		
26	59.8	2.6	409	4 US-09-528-794A-59		
27	59.8	2.6	409	4 US-09-569-098A-59		

QY 982 GCTTTATGCCATTCCATCATCAAGTTCTGCTGGGTATCTTAGGCT 1041
 Db 1 GENTTATGCCATTCCATCATCAAGTTCTGCTGGGTATCTTAGGCT 60
 QY 1042 CTCATGATCGGTTTCAATTCTCTGATGTTCTGGCAGTCGGTGG 1101
 Db 61 CTCATGATCGGTTTCAATTCTCTGATGTTCTGGCAGTCGGTGG 120
 QY 1102 ACHTGATGGTGTGATGCTTACACTTCTCCATTCTCAAGTCACCAT 1161
 Db 121 ACTTGATGGTGTGATGCTTACACTTCTCCATTCTCAAGTCACCAT 180
 QY 1162 AGCTATGCCATGAAAGAACGAACTGGAAATGAAAGGACCATTCAGTCATG 1221
 Db 181 AGCTATGCCATGAAAGAACGAACTGGAAATGAAAGGACCATTCAGTCATG 240
 QY 1222 TCCTCTCAAACATGAAAGAAGTCATGTTGATTCACATGGAGGTCTAACAGT 1281
 Db 241 TCCTCTCAAACATGAAAGAAGTCATGTTGATTCACATGGAGGTCTAACAGT 300
 QY 1282 CTAGGAGGCTGTATTTCATGTTCTGTTGAACTGCCTCACATGACAACATT 1341
 Db 301 CTAGGAGGCTGTATTTCATGTTCTGTTGAACTGCCTCACATGACAACATT 360
 QY 1342 AAAGTAAAGAAAAGATAAGAAAGATAAGAAACCTGAAATGATGATGTTGAGATAG 1401
 Db 361 AAAGTAAAGAAAAGATAAGAAAGATAAGAAACCTGAAATGATGATGTTGAGATAG 420
 QY 1402 AAGCAGTTGTCRAAGTGAATCTCAACTTCACAATGAAAGATAAGATACAGAT 1461
 Db 421 AAGCAGTTGTCAAATGATCTCACTTCACAATGAAAGATAAGATACAGAT 480
 QY 1462 GATGGAATGAGGCTTAACTGAGACTCACAGAACCCCTCCCTGATTCAG 1521
 Db 481 GATGGAATGAGGCTTAACTGAGACTCACAGAACCCCTCCCTGATTCAG 540
 QY 1522 CAGCCTGAGCTCTGGAGAGTCTGATGATGCTCATGCTCATCCACAGAGTC 1581
 Db 541 CAGCCTGAGCTCTGGAGAGTCTGATGATGCTCATGCTCATCCACAGAGTC 600
 QY 1582 TACATGAAATGACCAAGGGTGAAGGATAATGCACTTCACATTCCACATCA 1641
 Db 601 TACATGAAATGACCAAGGGTGAAGGATAATGCACTTCACATTCCACATCA 660
 QY 1642 CTCGCCAGTCAAGACATCAACCATGATGATGATGATTCAT 1701
 Db 661 CTCGCCAGTCAAGACATCAACCATGATGATGATTCAT 720
 QY 1702 CACCAACCAAAACCACTCTCACTGACACGACTCATGATCCAT 1761
 Db 721 CACCAACCAAAACCACTCTCACTGACACGACTCATGATCCAT 780
 QY 1762 AAAGATGCGGGTGGCCACTTGGCTGGATGATGGTGAATGGCTGACCAT 1821
 Db 781 AAAGATGCGGGTGGCCACTTGGCTGGATGATGGCTGACCAT 840
 QY 1822 TTGGCGTGGCTGACCAATTGGCTGATGAGGCTPATAGGGTTAAT 1881
 Db 841 TTCAAGCAGTGGCTCAATTGGCTGATGAGGCTPATAGGGTTAAT 900
 QY 1882 ACTCTGTTGCTGTTGCTGATGAGTGGCTCATGAAATTAGTGACTTGCTGTTA 1941
 Db 901 ACTCTGTTGCTGTTGCTGATGAGTGGCTCATGAAATTAGTGACTTGCTGTTA 960
 QY 1942 CTAAGGGTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 2001
 Db 961 CTAAGGGTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 1020
 QY 2002 GCGTATCTGGAAATGCCAGAAATTCTATGGCTCATGATGAAAGTTCTAG 2061
 Db 1021 GCGTATCTGGAAATGCCAGAAATTCTATGGCTCATGATGAAAGTTCTAG 1080

QY 2062 TGGATAATTGGACTTACCTGCTGGCTTATTCATGATGTTGCTGTTGATGGTACCT 2121
 Db 1081 TGATATTGGACTTACCTGCTGGCTTATTCATGATGTTGCTGTTGATGGTACCT 1140
 QY 2122 GAATGGTGCACAACTGATGTTGACCATGATGTCAGCTGGCTGGCTGGTATTCCTTTTA 2181
 Db 1141 GAATGGTGCACAACTGATGTTGACCATGATGTCAGCTGGCTGGCTGGTATTCCTTTTA 1200
 QY 2182 CAGAATGCTGGACTCTTGGAATTGGCTGATGTTGACTTATGGCTGATGTTGACAT 2241
 Db 1201 CAGAATGCTGGACTCTTGGAATTGGCTGATGTTGACTTATGGCTGATGTTGACAT 1259
 QY 2242 AAATGGTGTGTTGATTAATCTAG 2268
 Db 1260 AAATGGTGTGTTGATTAATCTAG 1285

RESULT 2
 US-08-311-023-3
 ; Sequence 3, Application US/08311023
 ; Patent No. 5693465
 ; GENERAL INFORMATION:
 ; APPLICANT: MANNING, David Lockwood
 ; NICOLSON, Robert Ian
 ; APPLICANT: GEE, Julia Margaret
 ; GREEN, Christopher Douglas
 ; APPLICANT: GREEN, Christopher Douglas
 ; TITLE OF INVENTION: METHODS FOR PREDICTING THE BEHAVIOUR OF
 ; BREAST TUMOURS
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Young & Thompson
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US08/311,023
 ; FILING DATE: 22-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PATCH, Andrew J.
 ; REGISTRATION NUMBER: Reg. No. 5693465 32,925
 ; REFERENCE/DOCKET NUMBER: WCM.56
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703/521-2297
 ; TELEX: 703/685-0573
 ; TELEFAX: 246425
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-311-023-3

Query Match 55.7%; Score 1263; DB 1; Length 2404;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1285; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 982 GGTTTATAGCCATTTCACATGTTCTGTCCTGCTGGGGTATCTTGTGCT 1041
 Db 1 GGTTTATAGCCATTTCACATGTTCTGTCCTGTCCTGCTGGGGTATCTTGTGCT 60
 QY 1042 CTAGATGCTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 2001
 Db 961 CTAGATGCTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 1020
 QY 1042 CTAGATGCTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 2061
 Db 1021 CTAGATGCTGGCATGACCGTTAACAGGAGCTGTCCTTAAATGCACTGAGCTG 1080

QY	1102	ACTTGTAGCTGAGCTTTACCTCTTCACATTCTCATGAACTTCAACCCAT	1161
Db	121	ACTTGTAGCTGAGCTTTACCTCTTCACATTCTCATGAACTTCAACCCAT	180
QY	1162	AGCATAGCCTAGAAACGGAATGAAAGGGACCACTTTGAGTACATCTG	1221
Db	181	AGCATAGCCTAGAAACGGAATGAAAGGGACCACTTTGAGTACATCTG	240
QY	1222	TCTTCTCAAACATAGAAAGAAAGTGCTTATTTGATTCACSTGGAAGGGCTCATACAGCT	1281
Db	241	TCTTCTCAAACATAGAAAGAAAGTGCTTATTTGATTCACSTGGAAGGGCTCATACAGCT	300
QY	1282	CTAGGGGCCCTGTTATTGATTTCTGTCGAACTGCTCACATTGATAAAGAAATT	1341
Db	301	CTAGGGGCCCTGTTATTGATTTCTGTCGAACTGCTCACATTGATAAAGAAATT	360
QY	1342	AAGATTAAGAAAGAAAGATCAGAAACCTGAAATGATGATGATGTTGAGGTTAAC	1401
Db	361	AAGATTAAGAAAGAAAGATCAGAAACCTGAAATGATGATGATGTTGAGGTTAAC	420
QY	1402	AACGATGTGTCCTAAAGTAAATCTCACTTCAAAATGAGTAAAGTAGATACAGAT	1461
Db	421	AACGATGTGTCCTAAAGTAAATCTCACTTCAAAATGAGTAAAGTAGATACAGAT	480
QY	1462	GATCGACTGAGGTTTACAGCAGACTCAAGACCCMCCACTTGTATGTCAG	1521
Db	481	GATCGACTGAGGTTTACAGCAGACTCAAGACCCMCCACTTGTATGTCAG	540
QY	1522	CACCCCTGCACTTGTGAAAGAAAGAGTCATGATGATGCTCATGAGGAACTG	1581
Db	541	CACCCCTGCACTTGTGAAAGAAAGAGTCATGATGATGCTCATGAGGAACTG	600
QY	1582	TGAAATTAATGTTACCCAGAGGTTGAAAGATAATGGCATTCACATTTCACATACA	1641
Db	601	TGAAATTAATGTTACCCAGAGGTTGAAAGATAATGGCATTCACATTTCACATACA	660
QY	1642	CTGGCCAGTTGAGATTCATTCAGATCAGACTACCATCATTCATCATCAT	1701
Db	661	CTGGCCAGTTGAGATTCATTCAGATCAGACTACCATCATTCATCATCATCAT	720
QY	1702	CACCAACCAAACCCATTCAGTCACGACCCGCTACTCAGGAGCTG	1761
Db	721	CACCAACCAAACCCATTCAGTCACGACCCGCTACTCAGGAGCTG	780
QY	1762	AAGATGCGCGGCACTTGGCTGTTGATGGTGTGATGGCTGCACAAAT	1821
Db	781	AAGATGCGCGGCACTTGGCTGTTGATGGTGTGATGGCTGCACAAAT	840
QY	1822	TTCAGGATGCGCTTACGCTTACGTTGCTGTTGATGGTGTGATGGCTGCACAAAT	1881
Db	841	TTCAGGATGCGCTTACGCTTACGTTGCTGTTGATGGTGTGATGGCTGCACAAAT	900
QY	1882	ACTCTGTGTTGCTGTTGATGAGTTGCTCATGAAATTGGTGTGCTGCTCA	1941
Db	901	ACTCTGTGTTGCTGTTGATGAGTTGCTCATGAAATTGGTGTGCTGCTCA	960
QY	1942	CTAAGGGTGGATGACCGTTAACAGGGCTGTCCTTATGGATTTGAGCTGCTG	2001
Db	961	CTAAGGGTGGATGACCGTTAACAGGGCTGTCCTTATGGATTTGAGCTGCTG	1020
QY	2002	GGTATCTGGATGCCAACGAAATTCTATGGTCATATGGTAAATGTTCTATG	2061
Db	1021	GGTATCTGGATGCCAACGAAATTCTATGGTCATATGGTAAATGTTCTATG	1080
QY	2062	TGGTATTTGCTCACTTACTGCTGGTTATCTGTTGCTGTTGATGGTACCT	2121
Db	1081	TGGTATTTGCTCACTTACTGCTGGTTATCTGTTGCTGTTGATGGTACCT	1140
QY	2122	GAATGCTGCAATTGATGCTGACCATGAACTAGCCCTGGGTATTCTTTTA	2181
Db	1141	GAATGCTGCAATTGATGCTGACCATGAACTAGCCCTGGGTATTCTTTTA	1200
QY	2182	CAGATGCTGGATGCTTGGTTGGAAATTGTTACTTATTCCTAATTGACAT	2241

; Sequence 65, Application US/08990571
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-990-571-65

Query Match 2.6%; Score 59.8; DB 3; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

RESULT 8
US-09-728-784A-65/C
; Sequence 65, Application US/09528784A
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Boughton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICRIDI INFECTION
; FILE REFERENCE: 210121.426C4
; CURRENT APPLICATION NUMBER: US/09/528,784A
; CURRENT FILING DATE: 2000-03-17
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 65
; LENGTH: 342

RESULT 9
US-09-569-098A-65/C
; Sequence 65, Application US/09569098A
; Patent No. 656433
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Boughton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Homer, Mary
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICRIDI INFECTION
; FILE REFERENCE: 210121.426C5
; CURRENT APPLICATION NUMBER: US/09/569, 098A
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 65
; TYPE: DNA
; ORGANISM: Babesia microti
; US-09-569-098A-65

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

Query Match 2.6%; Score 59.8; DB 4; Length 342;
Best Local Similarity 65.2%; Pred. No. 3.6e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 268 ATCCATATAACCATGACCAGCACATCACTCGAACCGAACATGACAGCAG 327
Db 210 AACAGTTCACTGGCCACACGCTTCACTAGGCCAACAGCTCAC 151

RESULT 10
US-08-990-571-60/C
; Sequence 60, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICRIDI INFECTION
; FILE REFERENCE: 210121.426C4
; CURRENT APPLICATION NUMBER: US/09/528,784A
; CURRENT FILING DATE: 2000-03-17
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY

STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZLP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/990,571
 FILING DATE: 11-DEC-1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 351 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-990-571-60

Query Match 2.6%; Score 59.8; DB 3; Length 351;
 Best Local Similarity 65.2%; Pred. No. 3.6e-07;

Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 268 ATCCATATAACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 327
 Db 210 AACAGCTTCACTAGCCACAGCTCACTAGGCCACAGCTCACTAGCCACAG 151

QY 328 CGTCACTCGACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 387
 Db 150 CTTCACATGAGCATCACTAGACGAGCATCACTGTGACATGAGTTAC 91

QY 388 TCTCACATAATCAT 402
 Db 90 TAGGCCACAGCTT 76

RESULT 11
 US-09-528-784A-60/C
 ; Sequence 60, Application US/09528784A
 ; Patent No. 6451315
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Homer, Mary
 ; APPLICANT: Secretst, Heather
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; AND TREATMENT OF B. MICRIDI INFECTION
 ; FILE REFERENCE: 210121.426C5
 ; CURRENT APPLICATION NUMBER: US/09/569,098A
 ; CURRENT FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 60

Query Match 2.6%; Score 59.8; DB 4; Length 331;

Best Local Similarity 65.2%; Pred. No. 3.6e-07;
 Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 268 ATCCATATAACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 327
 Db 210 AACAGCTTCACTAGCCACAGCTCACTAGGCCACAGCTCACTAGGCCACAG 151

QY 328 CGTCACTCGACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 387
 Db 150 CTTCACATGAGCATCACTAGACGAGCATCACTGTGACATGAGTTAC 91

QY 388 TCTCACATAATCAT 402
 Db 90 TAGGCCACAGCTT 76

RESULT 12
 US-09-569-098A-60/C
 ; Sequence 60, Application US/09569098A
 ; Patent No. 656943
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Homer, Mary
 ; APPLICANT: Secretst, Heather
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; AND TREATMENT OF B. MICRIDI INFECTION
 ; FILE REFERENCE: 210121.426C5
 ; CURRENT APPLICATION NUMBER: US/09/569,098A
 ; CURRENT FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 60

Query Match 2.6%; Score 59.8; DB 4; Length 331;

Best Local Similarity 65.2%; Pred. No. 3.6e-07;
 Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 268 ATCCATATAACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 327
 Db 210 AACAGCTTCACTAGCCACAGCTCACTAGGCCACAGCTCACTAGGCCACAG 151

QY 328 CGTCACTCGACCATGAGCATCACTAGACGAGCATCACTGTGACATGAG 387
 Db 150 CTTCACATGAGCATCACTAGACGAGCATCACTGTGACATGAGTTAC 91

QY 388 TCTCACATAATCAT 402
 Db 90 TAGGCCACAGCTT 76

RESULT 13
 US-08-390-571-63/C
 ; Sequence 63, Application US/08990571
 ; Patent No. 6214971
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G. et al.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

Query Match 2.6%; Score 59.8; DB 4; Length 351;
 Best Local Similarity 65.2%; Pred. No. 3.6e-07;
 Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,571
; FILING DATE: 11-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mak, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)682-4900
; TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-990-571-63

Query Match 2.6%; Score 59.8; DB 3; Length 356;
Best Local Similarity 65.2%; Pred. No. 3.7e-07;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 268 ATCCATACACATGACCAGAACATCACTCGAACAGCATCTGAGCCACCTGAG 327
Db 210 AACAGTTCACATGGCCACAGTTCACTAGGCCACCCACTAGGCCACAG 151

Qy 328 CGTCACTGAGCCATTGAGCATCTAGAACAGGAGCTACACTCTGACCATCAC 387
Db 150 CTTCACTAGGCCACCCGTCACAGGTTCACTAGGCCACCCACAGCTCAC 91

Qy 388 TCTACCATANTCAT 402
Db 90 TAGGCCACAGCTT 76

RESULT 14
US-09-558-784A-63/c
; Sequence 63, Application US/09528784A
; Patent No. 6451315
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Sleath, Paul R.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.426C4
; CURRENT APPLICATION NUMBER: US/09/528,784A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Babesia microti
US-09-558-784A-63

Query Match 2.6%; Score 59.8; DB 4; Length 356;
Best Local Similarity 65.2%; Pred. No. 3.7e-07; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 268 ATCCATACACATGACCAGAACATCACTCTGAGCCACCTGAGCATGATCAC 387
Db 210 AACAGTTCACATGGCCACAGTTCACTAGGCCACCCGTCACAGGTTCAC 151

Qy 268 ATCCATACACATGACCAGAACATCACTCTGAGCCACCTGAGCATGATCAC 387
Db 210 AACAGTTCACATGGCCACCCGTCACAGGTTCAC 151

Qy 328 CGTCACTGAGCCATTGAGCATCTAGAACAGGAGCTACACTCTGACCATCAC 327
Db 150 CTTCACTAGGCCACCCGTCACAGGTTCACTAGGCCACCCACAGCTCAC 91

Qy 388 TCTACCATANTCAT 402
Db 90 TAGGCCACAGCTT 76

Search completed: September 12, 2003, 16:55:42
Job time : 128.286 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-642-034-4

Perfect score: 2268

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Gapop 10.0 , Gapext 1.0

Searched: 1632420 seqs, 1213878141 residues

Total number of hits satisfying chosen parameters: 3264840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
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 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2222	98.0	2744	14	US-10-198-846-13805 Sequence 170, App
3	2220.4	97.9	3537	14	US-10-198-846-10007 Sequence 10007, App
4	2198	96.9	3586	14	US-10-176-247-51 Sequence 51, App
5	1141.4	50.3	1193	10	US-09-525-300-591 Sequence 591, App
6	900.4	39.7	1449	14	US-10-198-846-10321 Sequence 10321, App
7	694.2	30.6	1032	14	US-10-198-846-13805 Sequence 13805, App
8	578.4	25.5	606	14	US-10-198-846-8407 Sequence 8407, App
9	335.6	14.8	366	11	US-09-918-995-30283 Sequence 30283, App
10	331.8	14.6	905	14	US-10-198-846-7874 Sequence 7874, App
11	319.2	14.1	337	14	US-10-198-846-75020 Sequence 250, App
12	319	14.1	4417	12	US-09-814-53-22020 Sequence 22020, App
13	319	14.1	5330	9	US-09-789-561-14 Sequence 14, App
14	268	11.8	721	14	US-10-198-846-2288 Sequence 9288, App
15	253	11.2	504	14	US-10-198-846-4455 Sequence 1445, App
16	241.2	10.6	625	14	US-10-198-846-10373 Sequence 10373, App

ALIGNMENTS

```

RESULT 1
US-10-171-581-170
; Sequence 170, Application US/10171581
; General Information:
;   Applicant: Dai, Hongsye
;   Inventor: Linsley, Peter
;   Title of Invention: Signature Genes in Chronic Myelogenous Leukemia
;   Current Application Number: US/10-171-999
;   Current Filing Date: 2002-06-14
;   Prior Application Number: 60/298, 914
;   Prior Filing Date: 2001-06-18
;   Number of Seq ID NOS: 366
;   SEQ ID NO 170
;   LENGTH: 2744
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   Publication Information:
;     Database Accession Number: U41060
;     Database Entry Date: 2001-06-18
;     US-10-171-581-170

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QY	181	TCTACCGCTATGGAAAATTATTCTTGTCACTGAGGGTCAGAAAATTACTCAA	240	QY	1261	ACGGAAAGGGCTAACACCTAGGGCTGATTICATGTTTGTGACATGTC	1320
Db	318	TCTACCGCTATGGAAAATTATTCTTGTCACTGAGGGTCAGAAAATTACTCAA	377	Db	1380	ACGGAAAGGGCTAACACCTAGGGCTGATTICATGTTTGTGACATGTC	1439
QY	241	AATATGGCATGATAAATTAAAGAAATCCATAACCATGACCACTCA	300	QY	1321	CACATGATCAAACATTAAAGATAAGAAAGAACCTGAAAT	1380
Db	378	AATATGGCATGATAAATTAAAGAAATCCATAACCATGACCACTCA	437	Db	1440	CACATGATCAAACATTAAAGATAAGAAAGAACCTGAAAT	1499
QY	301	GACCAGGATCACTCGACCATGAGCCTACTGACCCATGACAC	360	QY	1381	GATGATATGGGATTAAGAGCAGTGTCCAGTGAATGTCACATTCAACAT	1440
Db	438	GACCAGGATCACTCGACCATGAGCCTACTGACCCATGACAC	497	Db	1500	GATGATATGGGATTAAGAGCAGTGTCCAGTGAATGTCACATTCAACAT	1559
QY	361	GACCAACACTGACCATGATCACTCACCATAATCAGCTCTTGSTA	420	QY	1441	GAGGAGAACTGATAAGATGACGAACTGAACTTACAGCAGACTCAASAG	1500
Db	498	GACCAACACTGACCATGATCACTCACCATAATCAGCTCTTGSTA	539	Db	1560	GAGGAGAACTGATAAGATGACGAACTGAACTTACAGCAGACTCAASAG	1619
QY	421	AGCGAAAAGGCTTGTGCCAGACCATGACTGAGTTCAGGTAAGAAC	480	QY	1501	CCCTCCACATTGATTCTAGGACCTGACTCTGGAGAAAGGGCTGATAGCT	1560
Db	540	AGCGAAAAGGCTTGTGCCAGACCATGACTGAGTTCAGGTAAGAAC	599	Db	1620	CCCTCCACATTGATTCTAGGACCTGACTCTGGAGAAAGGGCTGATAGCT	1679
QY	481	AGCGAGGAAAGGGCTACCGACAGAACATCCAGTGTAGGAGTGCAGAC	540	QY	1561	CAGCCTACATCCACAGGAACTGATAATGAAATGCTACACCATGAC	1620
Db	600	AGCGAGGAAAGGGCTACCGACAGAACATCCAGTGTAGGAGTGCAGAC	659	Db	1680	CAGCTATTCACAGAACTGATAACATGAAATGCTACACCATGAC	1739
QY	541	AGTGTTAGTGTAGTGTAGTGTAACTGACCTGACACTGCTCTGAGAAC	600	QY	1621	CATTCAATTCCAGATACACTGSCCACTGAGCAGATCTATTACACCATGAC	1680
Db	660	AGTGTTAGTGTAGTGTAGTGTAACTGACCTGCTCACACGTCAGAAC	719	Db	1740	CATTCAATTCCAGATACACTGSCCACTGAGCAGATCTATTACACCATGAC	1799
QY	601	TCTCTAGAACAAATTAGAGCCTCAAGACCTGCTCCAAAGATGTACAGC	660	QY	1681	TACCATATATTCTCATATCACCAACCAACATCAGTCAGCTCAGCCAG	1740
Db	720	TCTCTAGAACAAATTAGAGCCTCAAGACCTGCTCCAAAGTGTAGCAGC	779	Db	1800	TACCATATATTCTCATATCACCAACCAACCATCAGTCAGCTCAGCCAG	1859
QY	661	TCCAATCACCAGTGTACATCAACAGGCTGAGCTGAAACCTGCTCTGAGAAC	720	QY	1741	CGTACTCTCGGGAGAGTGAAGATGAAAGTGCCTGATGTTGATA	1800
Db	780	TCCAATCACCAGTGTACATCAACAGGCTGAGCTGAAACCTGCTCTGAGAAC	839	Db	1860	CGTACTCTCGGGAGAGTGAAGATGAAAGTGCCTGATGTTGATA	1919
QY	721	AATGAACTCTGTGAGGAGCCGAAAGGGCTTATTCAGAACAGAAAT	780	QY	1801	ATGGTAGCCATTCAGGATGCCATTGCAATTTGCTTACTGAA	1860
Db	840	AATGAACTCTGTGAGGAGCCGAAAGGGCTTATTCAGAACAGAAAT	899	Db	1920	ATGGTAGCCATTCAGGATGCCATTGCAATTTGCTTACTGAA	1979
QY	781	CCTCAGAGGTTCATGTCATCAAACTGACATTCAGGCAATGCCATT	840	QY	1861	GGCTTATCAAGTGGTTAGTACTCTGCTGTCATGAGTGTCCCTCATGAA	1920
Db	900	CCTCAGAGGTTCATGTCATCAAACTGACATTCAGGCAATGCCATT	959	Db	1980	GGCTTATCAAGTGGTTAGTACTCTGCTGTCATGAGTGTCCCTCATGAA	2039
QY	841	CCCTGAACTGCAACAGGTCACTAUCCTCTGTCAGGCAATGCCATT	900	QY	1921	TAGGTGACTGCGTTATCTAAAGCTGCGCATGACCTGCTCTTAT	1980
Db	960	CCCTGAACTGCAACAGGTCACTAUCCTCTGTCAGGCAATGCCATT	1019	Db	2040	TAGGTGACTGCGTTATCTAAAGCTGCGCATGACCTGCTCTTAT	2099
QY	901	AGATCTGTCGATCATACRAGTAAGAGGGCTGAACTCCTCAAAACCTATCA	960	QY	1981	AATGCTTGAGGATGCTGAGTGTGGCTATCTGGATGCAAGGATTCTGCTGT	2040
Db	1020	AGATCTGTCGATCATACRAGTAAGAGGGCTGAACTCCTCAAAACCTATCA	1079	Db	2100	AATGCTTGAGGATGCTGAGTGTGGCTATCTGGATGCAAGGATTCTGCTGT	2159
QY	961	TTACAAATAGCTGGCTGGTTATGCTCATTGATCACTGCTCTGCTGT	1020	QY	2041	TATGCTGAAATGTTCTATGCTGATTTCTACATGCTGGCTATCTGCTGT	2100
Db	1080	TTACAAATAGCTGGCTGGTTATGCTCATTGATCACTGCTCTGCTGT	1139	Db	2160	TATGCTGAAATGTTCTACATGCTGGCTATCTGCTGT	2219
QY	1021	CTGGGGTTACCTTGTGCTCTGACATGAACTGCTGCTGCTGCTG	1080	QY	2101	GCTCTGGTTATGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTG	2160
Db	1140	CTGGGGTTACCTTGTGCTCTGACATGCTGCTGCTGCTGCTGCTG	1199	Db	2220	GCTCTGGTTATGCTGACATGCTGCTGCTGCTGCTGCTGCTG	2279
QY	1081	CTTGTCGACTGGCTGGTTGGATGTTGCTGATGCTGCTGCTGCTG	1140	QY	2161	CGCTGGGGTATTCTTACAGAATGCTGGATGCTTGGTTGAAATTGTA	2220
Db	1200	CTTGTCGACTGGCTGGTTGGATGTTGCTGATGCTGCTGCTGCTG	1259	Db	2280	CGCTGGGGTATTCTTACAGAATGCTGGATGCTTGGTTGAAATTGTA	2339
QY	1141	TCTATGCAACTCACCATACTGACCATGAGAACCACTGAAATGAAAGA	1200	QY	2221	CTTATTCTGAAATTGAAATAAAATGGTTCTATAAATTCTG	2268
Db	1260	TCTATGCAACTCACCATACTGACCATGAGAACCACTGAAATGAAAGA	1319	Db	2340	CTTATTCTGAAATTGAAATAAACTGTTCTGCTATAAATTCTG	2387
QY	1201	GGACACTTTCAGCATCTGCTCTGACATGAAAGTGCCTATTGATCC	1260				
Db	1320	GGACACTTTCAGCATCTGCTCTGACATGAAAGTGCCTATTGATCC	1379				

RESULT 2

03-10-17-293-263

; Sequence 263, Application US10177293
; Publication No. US20030124128A1

Db	960	CCGCTGAATCACAAGAGTCACATCTGTGCCAGCCATCATCACACAAATTGATGCT	1019	QY	1981	AATGCATTTGTCAAGCCATGCTGGCTATCTTGGAAATGGCACAGGAATTTCATGGCAT	2040
QY	901	AGATCTTGTCGATTCATACAGTGAAGAAGCTGAATCCTCTCRAAGACTATICA	960	Db	2100	AATGCATTTGTCAAGCCATGCTGGGTATCTTGGAAATGGCACAGGAATTTCATGGCAT	2159
Db	1020	AATCTCTGTCGATTCACAGTGAAGAAGCTGAATCCTCTCRAAGACTATICA	1079	QY	2041	TATGCCTGAAATGTTCTAATGGTATTCATGATGTT	2100
QY	961	TAACATTAATGCTCGTGGTGGTGGTTATGCCATTTCATCATGTTCCCTCTCG	1020	Db	2160	TATGCCTGAAATGTTCTAATGGTATTCATGATGTT	2219
Db	1040	TAACATTAATGCTCGTGGTGGTGGTTATGCCATTTCATCATGTTCCCTCTCG	1139	QY	2101	GCTCTGGTGTGATGTTACCTGAAATGTCGACATGATGCTAGTGCACANGGATGTC	2160
QY	1021	CTGGGGTTATCTTAGTGGCTCTCATGANTGGTGTAAATTTCCTGAGTTTC	1080	Db	2220	GCTCTGGTGTGATGTTACCTGAAATGTCGACATGATGCTAGTGCACANGGATGTC	2279
Db	1140	CTGGGGTTATCTAGTGGCTCTCATGANTGGTGTAAATTTCCTGAGTTTC	1199	QY	2161	CGCTGGGGTATTCCTTACAGAATGCTGGGAGCTTGGGTTGGAAATTGTTGTA	2220
QY	1081	CTGGGGACTGGCGTGGTGGACTTACCTTCCTCCAAAT	1140	Db	2280	CGCTGGGGTATTCCTTACAGAATGCTGGGAGCTTGGGTTGGAAATTGTTGTA	2339
Db	1200	CTGGGGACTGGCGTGGTGGACTTACCTTCCTCCAAAT	1259	QY	2221	CCTATTCATCATTGACATAAAATGTCGTTGTTGTAATAAATTCTG	2268
QY	1114	TCTCATGCAATGTCACACCATAGTCATAGCCTGAACTGGAAATGAAARGA	1200	Db	2340	CCTATTCATCATTGACATAAAATGTCGTTGTTGTAATAAATTCTG	2387
Db	1260	TCTCATGCAATGTCACACCATAGTCATAGCCTGAACTGGAAATGAAARGA	1319				
QY	1201	GGACCACTTTCAGTCATGTCCTCAAAATAGAAAAGTCCTATTGATTC	1260		RESULT 4		
Db	1320	GGACCACTTTCAGTCATGTCCTCAAAACAAAGAAAGTCCTATTGATTC	1379		US-10-176-847-51		
QY	1261	ACCTGAAAGGCTAACAGCTCTAGAGGCTCATTCATGTCCTGAGCATTC	1320		; Sequence 51, Application US/10176847		
Db	1380	ACCTGAAAGGCTAACAGCTCTAGAGGCTCATTCATGTCCTGAGCATTC	1439		; Publication No. US20030068636A1		
QY	1321	CTAACATGTCATCAAACAAATTAAAGATAAGAGAAAGAACAGGAAAT	1380		; GENERAL INFORMATION:		
Db	1440	CTAACATGTCATCAAACAAATTAAAGATAAGAGAAAGAACAGGAAAT	1499		; APPLICANT: Velby, Petter Ole		
QY	1381	GATGATGATGTTGAAATAAGAGACTTGTCCAGTTGATGTTCAACAAAT	1440		; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR		
Db	1500	GATGATGATGTTGAAATAAGAGACTTGTCCAGTTGATGTTCAACAAAT	1559		; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER		
QY	1441	GACCGAAAGTACATGACATGTCAGGCTGACTTCACAGACTCACAGAG	1500		; TITLE OF INVENTION: AND OVARIAN CANCER		
Db	1560	GACCGAAAGTACATGACATGTCAGGCTGACTTCACAGACTCACAGAG	1619		; FILE REFERENCE: MRL-039		
QY	1501	CCCTCCACATTGATTCTCAGGGCTGACTTCACGGGCTCATGATGCT	1560		; CURRENT APPLICATION NUMBER: US/10/176-847		
Db	1620	CCCTCCACATTGATTCTCAGGGCTGACTTCACGGGCTCATGATGCT	1679		; CURRENT FILING DATE: 2002-06-21		
QY	1561	CATGCTCATCACAAGAACATGACATGAAATGACCGAGGCTCATGATGCT	1620		; NUMBER OF SEQ ID NOS: 112		
Db	1680	CATGCTCATCACAAGAACATGACATGAAATGACCGAGGCTCATGATGCT	1739		; SOFTWARE: FastSeq for Windows Version 4.0		
QY	1621	CATTCACATTCCAGATAACCTGGGCACTGAGCACTCATTCACCCATCATGAC	1680		; SEQ ID NO: 51		
Db	1740	CATTCACATTCCAGATAACCTGGGCACTGAGCACTCATTCACCCATCATGAC	1799		; LENGTH: 3586		
QY	1681	TACCATCATTCATCCTCATCACACCAAAACCACCATCTCACAGCCAG	1740		; TYPE: DNA		
Db	1800	TACCATCATTCATCCTCATCACACCAAAACCACCATCTCACAGCCAG	1859		; ORGANISM: Homo sapiens		
QY	1741	CGCTACTCTGGGGAGCTGAAAGATGCCGGCTGCCACTTGGCTGGATGCTGA	1800		Query Match	96.9%	
Db	1860	CGCTACTCTGGGGAGCTGAAAGATGCCGGCTGCCACTTGGCTGGATGCTGA	1919		Best Local Similarity	99.1%	
QY	1801	ATGGTGATGGCTGCACATTCAAGGATGGCTGAGCTGCTTACTGAA	1860		Matches	2248	
Db	1920	ATGGTGATGGCTGCACATTCAAGGATGGCTGAGCTGCTTACTGAA	1979		Score	21.98;	
QY	1861	GGCTTAACTGTTAAGTACTCTGTTCTGTCATGAGTCCTCTCATGAA	1920		Pred.	No.;	
Db	1980	GGCTTAACTGTTAAGTACTCTGTTCTGTCATGAGTCCTCTCATGAA	2039		Mismatches	0;	
QY	1921	TTGGTGACTTGTGTTCTACTAAAGGCTGGCATGACCGTTAACGGCTT	1980		Indels	20;	
Db	2040	TTGGTGACTTGTGTTCTACTAAAGGCTGGCATGACCGTTAACGGCTT	2099		Gaps	3;	

QY	AAAGGAAAGCTCTTGGCCAGACCATGACTAGATTCAGTAAGATCCTAGAAC 480	Db	CCCTCCCACTTTGGCTTCAAGGCCTGGAAGCTTGAGAAGAGTCATGATGCT 1560
665	AAAGGAAACCTTGTGCCAACCATGACTAGATTCAGTAAGATCCTAGAAC 724	Db	CCCTCCCACTTTGGCTTCAAGGCCTGGAAGCTTGAGAAGAGTCATGATGCT 1804
481	AGCCAGGGAGAGCTCACCGACATGACATGCCAGTGGTCAAGGATTCAGGAC 540	QY	CATGCTCATCACAGGAGTCAATGATACTACATGATACTACCAAGGGTGCAGATAATGCT 1561
725	AGCCAGGGAGAGCTCACCGACATGACATGCCAGTGGTCAAGGATTCAGGAC 784	Db	CATTACATTCCACGAGTCACTGGCCAGTCAAGACATCTACACCCATCTGAC 1620
541	AGTGTAGTGTCTAGTGTGACCTGAACTGTGACACACTGTCTCAAGAACAC 600	QY	CATTACATTCCACGAGTCACTGGCCAGTCAAGACATCTACACCCATCTGAC 1805
785	AGTGTAGTGTCTAGTGTGACCTGAACTGTGACACACTGTCTCAAGAACAC 844	Db	CATTACATTCCACGAGTCACTGGCCAGTCAAGACATCTACACCCATCTGAC 1865
601	TTCCTAGAGCAATAGAAGTCCAAAGATGTAAGGAGC 660	QY	CATTACATTCCACGAGTCACTGGCCAGTCAAGACATCTACACCCATCTGAC 1924
845	TTCCTAGAGCAATAGAAGTCCAAAGATGTAAGGAGC 904	Db	TACCATCATTCACCATCACACCACCAACCCACCCACAGTCAGCTGAGGATGATA 1621
661	TCCACCCACCCAGTCACTAAAGCCGGTGAGCGCTGGTAGAAACA 720	QY	TACCATCATTCACCATCACACCACCAACCCACCCACAGTCAGCTGAGGATGATA 1800
905	TCCACTCAACCCAGTCACTAAAGCCGGTGAGCGCTGGTAGAAACA 964	Db	TACCATCATTCACCATCACACCACCAACCCACCCACAGTCAGCTGAGGATGATA 1844
721	AATGAACTCTGAGTCAAGACAGTTCAGAAACACAATGAAAT 780	QY	CGTACTCTGGGAGTGCCTGAGAAATTCAGGAGGCTAGAAATGGCTGCTTATGAA 1860
965	AATGAACTCTGAGTCAAGACAGTTCAGAAACACAATGAAAT 1024	Db	ATGGGATGGCTGAGCAATTTAGGATGAAATGGCTGCTTATGAAATGGCTGTTTACGAA 2044
781	CCTCAGGAGTTCACTGACATCAAGCTGATCCATGGCATCCAGCT 840	QY	GTTTAACTAAGCTGTTAGTACTCTGGCTCTGTCATAGTGCCTCATAGTGCCTCAT 1881
1025	CCCTCAGGAGTTCACTGACATCAAGCTGATCCATGGCATCCAGCT 1084	Db	GTTTAACTAAGCTGTTAGTACTCTGGCTCTGTCATAGTGCCTCATAGTGCCTCAT 2105
841	CCCTGTAATGAAACAGAGTCAACTACTCGTCAGCCATDATCACCAAAATGATGCT 900	QY	TTAGGTGACTTGGCTGTTACTAAAGGCTGGCATGACGCTTAAGGAGGCTGTCCTTAT 1920
1085	CCCTGTAATGAAACAGAGTCAACTACTCGTCAGCCATDATCACCAAAATGATGCT 1144	Db	TTAGGTGACTTGGCTGTTACTAAAGGCTGGCATGACGCTTAAGGAGGCTGTCCTTAT 2105
901	AGATCTGTCGTCATCAACTGAAAGGAGCTGAAATCCTCAAGACCTATICA 960	QY	AAGCTTGGTCACTGAGCTGATGCTGGCTACTCTGGAAACGGAAATTCATGGCTCAT 1980
1145	AGATCTGTCGTCATCAACTGAAAGGAGCTGAAATCCTCAAGACCTATICA 1204	Db	AATGCAATTGTCAGCCATGTCGGTACTGCTGAAATTCATGGCTCATGGCTCAT 2164
961	TTACAAAATAGCCTGGTTTATAGCCATTCCATCATCASTTTCCTGCTCTG 1020	QY	TTAGCTAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 1924
1205	TTACAAAATAGCCTGGTTTATAGCCATTCCATCATCASTTTCCTGCTCTG 1264	Db	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2164
1021	CTGGGGTTACTTAGTGGCTTCATCAAAATGGTGTTCATGAAATTCTGAGATTC 1080	QY	GCTCTGGTGTGAAATGCTGAAATGGCTTACCTGATGCTGAAATGGCTTACCTGATGCTTATGCT 2160
1265	CTGGGGTTATTTAGTGGCTTCATAAATTCTGGTGTTCATGAAATTCTGAGATTC 1324	Db	GCTCTGGTGTGAAATGCTGAAATGGCTTACCTGATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1081	CTGGGGCACTGGCCTGGGACTTGGACTTTACCCCTCTCCAT 1140	QY	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1313	CTGGGGCACTGGCCTGGGACTTGGACTTTACCCCTCTCCAT 1384	Db	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1325	CTGGGGCACTGGCCTGGGACTTGGACTTTACCCCTCTCCAT 1384	QY	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1141	TCTCATGAACTCACCAATAGCCTAGCATGAGAACCCAATGAAATGAAAGA 1200	Db	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1385	TCTPATGAACTCACCAATAGCCTAGCATGAGAACCCAATGAAATGAAAGA 1444	QY	TAATGCTGAAATGTTCTGGCTGATTTGCAATGCTGAAATGGCTTACCTGATGCTTATGCT 2344
1202	GGACCACTTCACTGTCCTCAAAACATAGAAAGTGGCTTATTGATTC 1260	RESULT	5
		US-09-925-300-591	
		; Sequence 591, Application US/09/925300	
		; Patent No. US2010151681A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Craig Rosen	
		; ATTORNEY: Steve Rubin	
		; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies	
		; FILE REFERENCE: PAL01	
		; CURRENT APPLICATION NUMBER: US/09/925300	
		; CURRENT FILING DATE: 2001-08-10	
		; PRIOR APPLICATION NUMBER: PCT/US00/05988	
		; PRIOR FILING DATE: 2000-03-08	
		; PRIOR APPLICATION NUMBER: 60/124,270	
		; NUMBER OF SEQ ID NOS: 1890	
		; SOFTWARE: PatentIn Ver. 2.0	
		; SEQ ID NO: 511	
		; LENGTH: 119,3	
		; TYPE: DNA	

ORGANISM: Homo sapiens			
-09-925-300-591			
Query Match	50.3%	Score 1141.4;	DB 10; Length 1193;
Best Local Similarity	99.7%	Pred. No. 0;	
Matches 1139; Conservative	4;	Mismatches 0;	Indels 0; Gaps 0;
539 ACAGTGTAGTGTAGTGTAGCTCACTGTCACAGTGACCTGAGGAACCT 598		QY	1559 CTCATGCTCATCCACAGGAACTCTACATGAATGTAACCGAGGGTGCATCTTGAGAAGAAAGGGTGTAGAG 1618
1 ACAGTGTAGTGTAGTGTAGCTCACTGTCACAGTGACCTGAGGAACCT 60		Db	1021 CTCATGCTCATCCACAGGAACTCTACATGAATGTAACCGAGGGTGCAGAAG 1080
599 ACTTCATAGAACATAAGAGTCAAGACTCAGACCTGGAAACCTCTCCCAAAGATGTAAGCA 658		QY	1619 GCATTCACTATCCACGATACCTGGGCACTGAGGAACCTCTACACCACATG 1678
61 ACTTCATAGAACATAAGAGTCAAGACTCAGACCTGGAAACCTCTCCCAAAGATGTAAGCA 120		Db	1081 GCATTCACTATCCACGATACCTGGGCACTGAGGAACCTCTACACCACATG 1140
659 GCTCACCACCCAGTCACATCAAAGCCGGTGACCGGGTGGCTGTAGAAAA 718		RESULT 6	1679 ACT 1681
121 GCTCACACCCAGTCACATCAAAGCCGGTGACCGGGTGGCTGTAGAAAA 180		US-10-198-846-10321	
719 CAAATGAACTCTGAGTGTAGCTGGCCGAAAAGGCUTTATGTTACAGAACAAATGAAA 778		; Sequence 10321, Application US/10198846	
181 CAAATGAACTCTGAGTGTAGCTGGCCGAAAAGGCUTTATGTTACAGAACAAATGAAA 240		; Publication No. US2003009974A1	
779 ATCCCTGAGGAGGTTCAAGGATCAAACCTGATCATGCACTGAGGGATCAGG 838		; GENERAL INFORMATION:	
241 ATCCCTGAGGAGGTTCAAGGATCAAACCTGATCATGCACTGAGGGATCAGG 300		; APPLICANT: Lillie, James	
839 TTCCGCTAAATGCAACAGATTCAACTATCTGTCAGCATCATCAACAAATGATG 898		; APPLICANT: Xu, Yongyao	
301 TCCGCTGAATGCAACAGATTCAACTATCTGTCAGCATCATCAACAAATGATG 360		; APPLICANT: Wang, Youzhen	
899 CTAGATCTGTGTTGANTCATACAAAGTAAAGAGGCTGAATTCCTCAAAGACCTATT 958		; APPLICANT: Steinmann, Kathleen	
361 CTAGATCTGTGTTGANTCATACAAAGTAAAGAGGCTGAATTCCTCAAAGACCTATT 420		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
959 CATTACAATAACGCTGGGTTATAGCCATTCCATCATGATTCCTGGCTCT 1013		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
421 CATTACAATAAGCTGGGTTATAGCCATTCCATCATGATTCCTGGCTCT 480		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1019 TGGTGGGGTTATCTTAGTGSCCTCATGAATGGGTGTTTCAATTCCTCTGATT 1078		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
481 TGGTGGGGTTATCTTAGTGSCCTCATGAATGGGTGTTTCAATTCCTCTGATT 540		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1079 TCTTGTGGCACTGGCGGTGGACTTCAGTTGAGTGTGTTTACCTTCTGCC 1138		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
541 YCCYTGTGGCACTGGCGGTGGACTTCAGTTGAGTGTGTTTACCTTCTGCC 600		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
11139 ATTCTCANGCAGTCACCACTTACGTTCTCATGATGCACTGTTTCAATTCCTCTG 1198		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
601 ATTCTCANGCAGTCACCACTTACGTTCTCATGATGCACTGTTTCAATTCCTCTG 660		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1199 GAGGACCACTTTCAGTCATGTTCTCAAAACATAGAGAAAGTGCCTATTGATT 1258		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
661 GAGGACCACTTTCAGTCATGTTCTCAAAACATAGAGAAAGTGCCTATTGATT 720		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1259 CAAGTGGAAAGGCTTACACTCTAGGAGGCTGTATTTCATGTTCTGTTGAACTG 1318		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
721 CAAGTGGAAAGGCTTACACTCTAGGAGGCTGTATTTCATGTTCTGTTGAACTG 780		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1319 TCCCTCACATTGATCACACATTAAAGATAAGAGAAAGAGTCAAGAAACCTGAA 1378		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
781 TCCCTCACATTGATCACACATTAAAGATAAGAGAAAGAGTCAAGAAACCTGAA 840		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1379 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1438		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
841 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1439 ATGAGGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1498		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
901 ATGAGGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1499 AGCCCTCCACATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1553		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	
1327 TTGATCATAACATTAAAGATAAGAGAAAGATAACGAAACTGAAATGATGAT 1386		; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS	

; Sequence 8490, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIORITY NUMBER: 60/306,220
 ; PRIORITY FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 38054
 ; SEQ ID NO: 8490
 ; LENGTH: 606
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: 1..44..516..571..600..606
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-198-846-8490

Query Match 25.5%; Score 578.4; DB 14; Length 606;
 Best Local Similarity 99.0%; Pred. No. 1..8e-15;
 Matches 590; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1042 CTCATGAATGGGTGTTCAAAATTCTCCCTAGTTCTGCACACTGGCGTGGG 1101
 Db 11 CGATAAACGGGTGTTCAACCTCTCCACATTCCTCAGTCAGTCACCAT 1111
 QY 1102 ACTTCAGTGGTGTGCTTTCACCTCTTCACATTCCTCAGTCAGTCACCAT 1161
 Db 70 ACTTGAGTGGTGTGCTTTCACCTCTTCACATTCCTCAGTCAGTCACCAT 129
 QY 1162 AGTCATAGCCTGAGACCACTGAGACCAATGGAAATGAAAGGACCATTCATCTG 1221
 Db 130 AGTCATAGCCTGAGACCACTGAGACCAATGGAAATGAAAGGACCATTCATCTG 189
 QY 1222 TCTCTCAAACATAGAGAACAGTGCCTATTGATCAGTGAAGGCTTAACGCT 1281
 Db 190 TCTCTCAAACATAGAGAACAGTGCCTATTGATCAGTGAAGGCTTAACGCT 249
 QY 1282 CTAGGGCCGCTGTTACATTGATGTTGTTGAACTGTCMPCACATGTACAATTT 1341
 Db 250 CTAGGGCCGCTGTTACATTGATGTTGTTGAACTGTCMPCACATGTACAATTT 309

RESULT 10
 US-10-198-846-7874
 ; Sequence 7874, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; PRIORITY NUMBER: 60/306,220
 ; PRIORITY FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SEQ ID NO: 7874
 ; LENGTH: 905
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

QY	1209	TTCAGCAGTCGTCTCCAAACATAGAAGAAGTGCCTTAATGATCCACTGGAA	1268
Db	786	TCATGGCATGAAATTACAGTTTGGGAA	836
QY	1269	GGGTCTAACCGCTTCTGGGGCTGTATTTCATGTTCTCAATTAACTGAAACTGAA	1328
Db	837	AGACTGTGTCCTPAGGGCTTACTTCATGTTCAATTAACTGAAACTGAA	896
QY	1329	GATCAAACATTAAAGATAAGAAGAAGTGTATGAAACAGAACAGAA	1385
Db	897	GTTAACGCAACACACAAACACAAACACAAACACAAACACAAACAGAA	956
QY	1386	TGATGGGAGATTAGAACGGCTGTCGAATTAATTCACATTCAAAATGAGA	1445
Db	957	AGATCAACTTGTGGAAAGGCTTCAAGATCACAAAGTTAAACAAATCTCA	1016
QY	1446	GAATGAGTAAAGTGTGATGCAACTGAAGCTGAAGGTTTACAGGAGAC	1505
Db	1017	CTGGCTCAACTCAACCTCTCCGGAAACTGTACTGGTTCTGAGATGCGT	1076
QY	1506	CACTTGTATTCTTCAGAACGCTGCACTGGAAAGAAGAGGTCAATGATGAGCTGC	1565
Db	1077	TAATGAAACTGAACTGACAGATTAGGGCAAAAGATCCCTCTAAATACTT	1136
QY	1566	TCATGCCAGGAAAGCTCAATGATGCAAGGGTGAAGATAATGCCATTC	1625
Db	1137	TGTATGAAAGGGC-AAAATGAACTGATGTTGATGGGATATACATCC	1194
QY	1626	ACATTCCAGMTAACTCGCACTGAGTACATTCATCACACCATGATCA	1685
Db	1195	-CATGRCATGATCROCANGTCTGACATPAAACCACGGGGAGAACAAACTGTGT	1253
QY	1686	TCATATTCGATCATCACCCACCAAAACCCACATCTCAAGTGCACGCCACGCTTA	1745
Db	1254	GAGGAAGCATATCACCAGTGGACCACAAAGATCTCATCCATGCCCCGTGA	1313
QY	1746	CTCGCGAGCAAGATGCCGCGTGCGCACTTNGCTGTGATGATATGG	1805
Db	1314	TTCGGATCCGATCTGAAGAACAGGAATAGCTTATAGGCGGATATG	1373
QY	1806	TGATGGCTGCACAAATTAGCGATGGCCTAGCAATTGGCTCTTATGAGGCT	1865
Db	1374	GTATGGCATCCACAACTTCACTGATGATGGCTCGCAATTGTGGGATT	1433
QY	1866	ATAAAGGGTTAAGTACTCTGCTGCGTGTGCTGATGATTAGTAGT	1925
Db	1434	GACAGGGGAAACAGTACTCTATAGCGCTCTCCTGATGACATGATAGT	1493
QY	1926	TGACTGTGCTGTTCAACTAAGGGATGACCGCTTAAGCAGCAATGTTAATG	1985
Db	1494	AGATTTGCGAGTCCTCTTAAGGGCATCTTAAGCAGCAATGTTAATG	1553
QY	1986	ATGGTCAGCCATGCTGGCTATCUTGGAAATTTCTATGGCTTATATGC	2045
Db	1554	CCTCTGCGCAATGCTGCTTCAAGGGCATCTTAAGCAGACCTTGTGAT	1613
QY	2046	TGAAATGTTGTTAATGTTGATAATTGCTGGCTTAATCTGATGTTGCTT	2105
Db	1614	CAATACATCACACTGATGCTGCTGAGGGATGTCTCTATGAGCCCT	1673
QY	2106	GGTGTGATGGTACCTGGCAATGTCGACAGTTGTTGATGTTG	2159
Db	1674	GTGTGATGGTGCCTCCAGAARATGTCGTCGATGTTGATGTTG	1733
QY	2160	CGCTGGGGGTTTCAAGAATGCTGGATGCTTGGTTGGGAATTATGTT	2219
Db	1734	TCCGTGGGGGTTTCAAGAATGCTGGATGCTTGGTTGGGAATTATGTT	1793
QY	2220	ACTATTCCTAACATTGACATTAATGCTTGTGTTGTTAAATTCT	2266
Db	1794	GTGGATCCCTCTGATGAAATGTTGTTGACATCCCTTGTGATGTTG	1840

RESULT 13
US-09-789-561-14
; Sequence 14, Application US/09789561
; Patent No. US02006418A1
; GENERAL INFORMATION:
; APPLICANT: Ni, et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: PZ043P1
; CURRENT APPLICATION NUMBER: US/09-7789-561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIORITY NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIORITY NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 5330
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-789-561-14

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Qy	1029 TATCTTAGTGCTCTCATGAATGGGTGTTCAAAATTCTCGTGAAGTTCTGTGGC	10.9%	Mismatches 535;	Indels 36;	Gaps 6;
Db	1432 GATCTGGTCCATCATTAACAGGATGCTTCATACCTCTACATCTGTTGC				
Qy	1089 ATCGCGGTGGACTTTAGTGGTGTGCTTACACCTCTTCAACATTCTATGCC				
Db	1492 ATTAGCTGTGATAAAATAGTGGAGGCGCTTCACTGCCCATTCTAGGG				
Qy	1149 AACTCACCACTATCTCATGGCTATGAGAAACCGAACATGGAAATGAAAGGGCAACT				
Db	1552 TGGACATGATCACAGTCACAAATGGACA-----TGGCATGGACATTC				
Qy	1209 TTTAGCTATGCTCTGGGGCTGTCTCAACCATAGAAAGTGCATTGTTCTGTTA				
Db	1597 TCATGGACATGAACTAACAGTTTGGAGA-----TATGATGCTGTATGAA				
Qy	1269 GGTCTAACCTCTGGGGCTGTCTGGGGCTGTCTGTTAAGTGTCTCATTT				
Db	1646 AGGACTGTGCTCTGGGGCTTCTGTTCTGTTATCATGAACTGTTGAAT				
Qy	1329 GATCAACAAATTAAAGATAAGA--AGAAAAAGATCAGAAAACCTGAAATGATGA				
Db	1708 GTTTAACCTAACAAACAAAGAGAAATGAAATGTTATGAAACAAACAGCA				
Qy	1386 TGGTGGAGTTAGAACGATTGCTCAAGTATGATCTCACTTCACAAATGAGGA				
Db	1768 AGATCAACATTGGAAAGGCTTCAAGATCACAGTTAACAAATACAGGATCTGA				
Qy	1446 GAAGTAGATGATGAGTGAAGTGAAGTGAAGCTTACAGGCTTACAGGCTC				
Db	1828 CTTGGCTCAACTCAAGCTCTGGGAACTGATGACTCGGTGTTCTGAGATGACT				
Qy	1506 CCACTTGATCTCAGCAGCTGAGCTTCTGGAAAAGAGGTTCACTGATGCTCATGC				
Db	1888 TATGAAACTAACAGACAGATTAGGGCCAACAGATCCCTCTAAATACTCT				
Qy	1566 TATCCCGAGGCTCTGAGATATGTTACAGTCAACAGGCTGAAAGATAATGCGATTC				
Db	1946 TCTATGAAAGGGAG-AAAATAGACCTTCACAGTGTGTTACATACATACATT-				

LOCATION: 488, 493, 495, 504, 509, 519, 529, 536, 545, 547
 OTHER INFORMATION: n = A,T,C or G
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 552, 555, 559, 560, 564, 565, 578, 580, 581, 585, 587, 589,
 LOCATION: 590, 593, 594, 600, 604, 609, 611, 623, 625, 626, 627, 628,
 LOCATION: 629, 642, 643, 644, 647, 648, 651, 658, 664, 671, 673, 675, 676,
 LOCATION: 679, 681, 691, 694, 695, 696, 698, 703, 706, 712, 713
 OTHER INFORMATION: n = A,T,C or G
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 714, 718
 OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-9288

Query Match
 Best Local Similarity 11.8%; Score 268; DB 14; Length 721;
 Matches 294; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1806 TGATGGCTTCGACAAATTCCGGCATGGCTAACATGGCTTACTGARGCT 1855
 Db 2185 GGATGGCATCACAACTCAGTGGCTCCAAATGGCACTTGCTGGATT 2244
 QY 1866 ATCAAGTGTETTAAGTACTGTTGCTGTCATGATGAGTGTGATTAGG 1925
 Db 2245 GACAGGAAACAAGAAGRACTCTATGGCGTCTCTGTCAAGTGCACANGANTAG 2344
 QY 1926 TGACTTGCTGTTCTACTAAGGGCTGATGACCGTAAGCCTGTCCTTATATGC 1985
 Db 2305 AGATTTGGATGCTCTTCTTAAAGGAGGTGACTGTAAGAACATGTACACCT 2344
 QY 1986 ATTGGCAGGCACTCTGCCTGATGCTGAGGATTTCTATGGCTTATATGC 2045
 Db 2365 CCTCTGCTGATGAGCTCTACATGGCTCATGGCTAAAGGAGGTGACTGTAAG 2444
 QY 2046 TGAATAATGTTCTGATGGGATATTGGCAATTATGGCTTATTCATCTGGCTCT 2105
 Db 2425 CAATAACATACACTTGGACATTGCACTCATGTCAGGCAATGTCCTCTATG 2444
 QY 2106 GGTGATATGGTACCTTAAGGCTGACATGTGCTTATGGT-----CTATGACCAGTAGGTAG 2159
 Db 2485 GGTGGATATGCTTCAGAATGTTGCAATGGTGCATGGATGGTGAATGAGACANGCTT 2544
 QY 2160 CGGTGGATGTTCTTCAATGGTCAATGGTGGATTTGGATTGTGGTT 2249
 Db 2545 TCTCTGGGGCAATTCTCTCTCAATTAGGATGCTCTTGGATTGCTTATATGC 2604
 QY 2220 ACTTATTCATATGGACATAAATCGTTGCTGATAAATTTCT 2266
 Db 2805 GGTTGATGCTTAAAGGTTGACATGGTGGATGGTGAATCTGGTT 2651

RESULT 15
 US-10-198-846-1455/c
 Sequence 1455, Application US/1019846
 Publication No. US2003009974A1
 GENERAL INFORMATION
 APPLICANT: Lillie, James
 APPLICANT: Wang, Youzhen
 APPLICANT: Wang, Yongrui
 APPLICANT: Steinmann, Kathleen
 APPLICANT: Steinmann, Kathleen
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 THERAPY OF BREAST CANCER
 CURRENT APPLICATION NUMBER: US/10/198, 846
 FILE REFERENCE: MRI-049
 CURRENT FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/306, 220
 PRIOR FILING DATE: 2001-07-18
 NUMBER OF SEQ ID NOS: 14084
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO 9288
 LENGTH: 721
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 8, 11, 42, 262, 279, 324, 333, 337, 344, 346, 349, 352, 374,
 LOCATION: 361, 401, 403, 405, 407, 415, 417, 419, 421, 423, 425, 427, 429,
 LOCATION: 445, 454, 457, 458, 459, 464, 468, 469, 470, 473, 475, 477
 OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-1455

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Best	Local Similarity	253;	14;	504;
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		0;	Indels	15;
		Mismatches	Gaps	10;
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Db	497 AACCNAGCNAATGAAATAAAGAACCCACCTTTRACGCAATTGCTTC	438		
QY	1227 TC-AAACATAGAG-MAAGGGCTCAA-AAGCT	1281		
Db	437 TCNAAACATAGAGAAAGTGCTTGTGANTTCCAGTGGAAAGGTFAACCGCT	378		
QY	1282 CTAGAGGCCTGTATTCATTTCA-TTGTGAACTATGCC-TCACATTGATCAACA	1337		
Db	377 CTAGAGGCCTGTATTTAGTGTGAAATGCTCTCATTTGATCAACA	318		
QY	1338 ATTAAAGATAAGAAGAAAGAATCAGAAACCTGAAAATGATGATGATGATGAGAT	1397		
Db	317 ATTAAAGATAAGAAGAAAGAATCAGAAACCTGAAAATGATGATGATGAGAT	258		
QY	1398 TAAGAGCAGTGTCC-MAGTATGATTCACATT--CAACAAATGAGGAAGTAG	1453		
Db	257 TAAGAGCAGTGTCCAAAGTGAATGATGATCTCAACNTCCACAAANGAGGAAGTAG	198		
QY	1454 ATACAGATATGCACTGAAGCTTACGAGACTCACAGGCCTCCACTTG	1513		
Db	197 ATACAGATATGCACTGAAGCTTACGAGACTCACAGGCCTCCACTTG	138		
QY	1514 ATTCTCAGCAGCTGGAGCTGGAGAGAGGTCATGATAGCTCATGCTCAC	1573		
Db	137 ATTCTCAGCAGCTGGAGCTGGAGAGAGGTCATGATAGCTCATGCTCAC	78		
QY	1574 AGGAAGTC-TACATGATATGTAAC	1598		
Db	77 AGGAAGTCATGATATGTAAC	52		

Search completed: September 12, 2003, 22:12:52
 Job time : 529.999 secs

GenCore version 5.1.6
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Om protein - protein search, using sw mode1

Run on: September 12, 2003, 16:55:50 ; Search time 73 Seconds
(without alignments)
1641.624 Million cell updates/sec

Title: US-09-642-034-5
Perfect score: 4024

Sequence: 1 MARKSLLVILFALSVTNP.....FGIMLISIFEHKIVERINF 755

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 15872657 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4024	100.0	755	23	ABG61889	Prostate cancer-as
2	4024	100.0	755	23	AAM51198	Human breast cancer
3	4024	100.0	755	24	ABR48228	Human bladder cancer
4	4024	100.0	755	24	ABU56908	Lung cancer-associated
5	4020	99.9	755	23	ABG7649	Human protein, homologous LIV-1-166647
6	4017	99.8	755	22	AAE0706	Breast cancer-associated
7	4011	99.7	755	23	ABJ05550	Breast cancer-associated
8	3969	98.6	749	24	ABR47514	Oestrogen-regulate
9	3948	98.1	746	23	AAU74631	

WO200230268-A2.

PN WO200230268-A2.

XX XX

PD 18-APR-2002.

XX XX

PR 12-OCT-2001; 2001W0-US32045.

PR 08-DEC-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733288.

PR 13-OCT-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733288.

(EOSB-) EOS BIOTECHNOLOGY INC.

Rank	Score	Query	Match	Length	DB ID	Description
10	3906	97.1	3902	22	ABJ37050	Human breast cancer
11	3902	97.0	2205	12	AAE07205	Human LIV-1 protein encoded by
12	2188	54.8	431	19	AAW34504	Oestrogen-regulate
13	2188	54.4	431	17	AAR9004	Human prostate can-
14	1972	49.0	397	21	AAB55953	Human gene 4 encod
15	1337	33.2	831	22	AAB87345	Human albumin fusi-
16	1337	33.2	831	23	ABG65404	Novel human protei-
17	1337	33.2	831	23	ABB97347	Oestrogen-regulate
18	1328.5	33.0	829	23	AAM51199	Mouse breast cancer
19	1153	28.7	998	23	AAM51199	Human adipocyte Se-
20	1066	26.5	195	24	ABU70466	Oestrogen-regulate
21	734	18.2	528	23	ABB61691	Drosophila melanog-
22	715	17.8	684	23	AAU74625	Oestrogen-regulate
23	715	17.8	684	23	AAU74625	Human transmembran-
24	657.5	16.3	540	21	AAU51930	Oestrogen-regulate
25	652.5	16.2	535	23	AAU74632	Human albumin fusi-
26	632.5	15.7	492	23	ABG65035	Human secreted pro-
27	632.5	15.7	492	23	AAU91358	Oestrogen-regulate
28	632.5	15.7	492	23	AAU74621	Human HCMV induce-
29	632.5	15.7	531	20	AAU03376	Human cell cycle a-
30	632.5	15.7	537	22	ABP6046	Oestrogen-regulate
31	632.5	15.7	537	23	AAU74622	Oestrogen-regulate
32	607.5	15.1	540	22	ABB71162	Drosophila melanog-
33	595.5	14.8	519	23	AAU74622	Oestrogen-regulate
34	593	14.5	460	22	AAG81272	Human polypeptide
35	583	14.5	460	23	AAU74624	Human AFP protein
36	583	14.5	460	23	ABP04723	Oestrogen-regulate
37	580.5	14.4	462	23	AAU74623	Human PP3105 prote-
38	575.5	14.3	517	23	AAU74622	Oestrogen-regulate
39	575.5	14.3	519	22	ABB71162	Drosophila melanog-
40	575.5	14.3	519	23	AAU74622	Oestrogen-regulate
41	573	14.2	393	22	AAU95161	Human protein sequ-
42	573	14.2	406	23	ABR89582	Human polypeptide
43	552	13.7	660	23	AAU74620	Oestrogen-regulate
44	552	13.7	691	23	ABP43482	Human secreted pro-
45	543.5	13.5	622	23	ABP64821	Human protein SEQ

ALIGNMENTS

RESULT 1	ID	NAME	DESCRIPTION
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	AC	ABG61889;	
	XX	XX	(first entry)
	DT	DT	
	XX	XX	Prostate cancer-associated protein #90.
	DE	DE	
	XX	XX	KW
	OS	OS	Mammalia.
	XX	XX	
	PN	PN	WO200230268-A2.
	XX	XX	
	PD	PD	18-APR-2002.
	XX	XX	
	PR	PR	12-OCT-2001; 2001W0-US32045.
	PR	PR	
	08-DEC-2000	08-DEC-2000	2000US-0687576.
	PR	PR	
	13-OCT-2000	13-OCT-2000	2000US-0687576.
	PR	PR	
	08-DEC-2000	08-DEC-2000	2000US-0733288.
	PR	PR	
	24-FEB-2001	24-FEB-2001	2001W0-US32045.
	PR	PR	
	16-MAR-2001	16-MAR-2001	2001US-263557P.
	PR	PR	
	2001US-276588P.	2001US-276588P.	
	PR	PR	
	06-APR-2001	06-APR-2001	2001US-281922P.
	PR	PR	
	24-APR-2001	24-APR-2001	2001US-286141P.
	PR	PR	
	30-APR-2001	30-APR-2001	2001US-0847046.
	PR	PR	
	04-MAY-2001	04-MAY-2001	2001US-288589P.
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DT	12-JUN-2003 (first entry)		
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DE	Human bladder cancer associated protein sequence		
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KW	Human; bladder cancer; cytostatic; gene therapy;		
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GS	Homo sapiens.		
XX			
PN	WO2003003906-A2.		
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PD	16-JAN-2003.		
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PP	03-JUL-2002; 2002WO-US221338.		
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PR	03-JUL-2001; 2001US-302814P.		
PR	03-AUG-2001; 2001US-310099P.		
PR	08-NOV-2001; 2001US-343705P.		
PR	13-NOV-2001; 2001US-350666P.		
PR	12-APR-2002; 2002US-372246P.		
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PA	(EOSB) - EOS BIOTECHNOLOGY INC.		
XX			
PI	Mack DH, Aziz N;		
XX			
DR	WPI: 2003-201532/19.		
XX			
DR	N-PSDB; ACC51044.		
XX			
PT	Detecting a bladder cancer-associated transcript patient, comprising contacting a biological sample with a bladder cancer-associated polynucleotide or anti-bladder cancer-associated transcript in a cell from a patient.		
XX			
PS	Claim 10; Page 290; 307pp; English.		
XX			
CC	The present invention describes a method for detecting a cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a probe that selectively hybridises to a sequence that is complementary to a sequence (see ACC50951 to ACC51059). The probe encodes the human bladder cancer-associated protein ABR48242. Bladder cancer-associated sequences have cytostatic activities, and can be used in an anti-cancer vaccine production. The method can be used for diagnosing or treating bladder cancer, such as compounds that modulate nucleic acid molecules from the present invention. The nucleic acid molecules can be used for various screening and diagnostic methods, and for and/or antisense/inhibition applications.		
XX			
SQ	Sequence 755 AA;		
QY	Query Match 100.0%; Score 4024; DB 24 Best Local Similarity 100.0%; Pred. No. 0; Matches 755; Mismatches 0;		
DB	1 MARKLSVLLIFALSVTPNPLHEKAAFPQTTEKISPN 1 MARKLSVLLIFALSVTPNPLHEKAAFPQTTEKISPN		
QY	61 FYRGGENNSLSYEGERKLQLONGIDKIKRHHTHDHDDH		

QY	421	TWKSLTALGGLYFMFLIVEHYLTLLKQFKDKKKKNOKKPENDDOVEIKKQSKYESOLSTN	480	DR WPI: 2002-590675/63.
Db	421	TWKSLTALGGLYFMFLIVEHYLTLLKQFKDKKKKNOKKPENDDOVEIKKQSKYESOLSTN	480	DR N-SDDB; AB59544.
QY	481	EETKDTDDRTGYLRADSQPESHDQSOPAVLEEYEMIAHAPQEVNEYPRGKNC	540	XX Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating disorders associated with aberrant expression or activity of SECX/NOVX nucleic acids and proteins e.g., diabetes
Db	481	EETKDTDDRTGYLRADSQPESHDQSOPAVLEEYEMIAHAPQEVNEYPRGKNC	540	XX
QY	541	RSHFIDITLGQSDDLIHHHDYHTLHHHHQNHPHSQSYSRREELDAGTATLWAVI	600	XX Claim 16; Page 81; 443pp; English.
Db	541	RSHFIDITLGQSDDLIHHHDYHTLHHHHQNHPHSQSYSRREELDAGTATLWAVI	600	XX The invention discloses the isolated human polypeptides, and
QY	601	MGDGLAHNFSDGLAAGAFTEGLSSLSTSVAFCHELPHELDFAVLKGATVKAVLY	660	CC poly nucleotides encoding them, that have been designated SECX and NOVX.
Db	601	MGDGLAHNFSDGLAAGAFTEGLSSLSTSVAFCHELPHELDFAVLKGATVKAVLY	660	CC The polypeptides can be used for treating, or delaying, the onset of an
QY	661	NALSAMLAIGNATGIFTGHYAENNSWIFALTAGLFMYALDVMPEMLNDASDHGCS	720	CC angiogenically-associated disorder or treating a pathological state in a
Db	661	NALSAMLAIGNATGIFTGHYAENNSWIFALTAGLFMYALDVMPEMLNDASDHGCS	720	CC subject, preferably a mammal. They can also be used in determining the
QY	721	RWGFFFLQAGMILGRCMILLISIEHKTYFRNF	755	CC presence or, or predisposition to, a disease associated with altered
Db	721	RWGFFFLQAGMILGRCMILLISIEHKTYFRNF	755	CC levels of the polypeptides and poly nucleotides of any one of the 12
QY	ABG76949	standard; Protein; 755 AA.		CC sequences (SEC1-12), for raising antibodies for identifying an agent
XX	ABG76949;			CC that binds to, or that modulates the expression or activity of the
AC				CC polypeptide, for treating or preventing a NOVX associated disorder
XX				(NOV1-8) and as a pharmaceutical composition comprising the polypeptide,
DT	05-NOV-2002	(first entry)		CC (NOV1-8) and as a pharmaceutical composition comprising the polypeptide,
XX				CC poly nucleotide or the antibody. The polypeptides and poly nucleotides are
DE				CC useful in diagnostic applications where their amounts are assessed, or
KW				CC for the manufacture of a medicament (e.g. gene therapy) for treating or
KW				CC preventing disorders or syndromes such as developmental disorders, immune
KW				CC diseases, signal transduction pathway disorders, metabolic disorders,
KW				CC feeding disorders (including obesity), wasting disorders,
KW				CC neurodegenerative disorders (including Alzheimer's disease and
KW				CC Parkinson's disease), behavioural disorders, allergies, asthma,
KW				CC atherosclerosis, cardiomopathy, angina pectoris, autoimmune diseases,
KW				CC retinal disease, cirrhosis, diabetes, infections, autoimmune disease (bacterial,
KW				CC fungal, protozoal and viral e.g. human immunodeficiency virus, HIV),
KW				CC cancer (e.g. prostate cancer), hypertension, hypotension, multiple
KW				CC sclerosis, urinary retention, osteoporosis, Crohn's disease, ulcers,
KW				CC neurological disorders (e.g. anxiety), haemophilia or cirrhosis. They
KW				CC may also be used as immunogens to produce antibodies specific for the
KW				CC invention, and as vaccines. Further, they are useful for screening
KW				CC potential agonist and antagonist compounds. The sequences presented in
KW				CC ABG76949-AB676556 are the human SEC1-12 and NOV1-8 proteins.
XX				XX Sequence 755 AA;
QY	ABG76949	standard; Protein; 755 AA.		Query Match 99.9%; Score 4020; DB 23; Length 755;
XX				Best Local Similarity 99.9%; Pred. No. 0;
AC				Mismatches 0; Indels 0; Gaps 0;
XX				Matches 754; Conservative 1;
DE				Db 1 MARKLYSTILTFALSVINPLBLKAAPOTTEKISNWEGINDLA-STROYBLQL 60
KW				Db 1 MARKLYSTILTFALSVINPLBLKAAPOTTEKISNWEGINDLA-STROYBLQL 60
KW				Db 1 FRYGYENNLSVEGFRKLQNLGIDKTKRHTHDDHSDHEHSDHEHSDH 120
KW				Db 61 FRYGYENNLSVEGFRKLQNLGIDKTKRHTHDDHSDHEHSDHEHSDH 120
KW				QY 1 MARKLYSTILTFALSVINPLBLKAAPOTTEKISNWEGINDLA-STROYBLQL 60
KW				QY 1 MARKLYSTILTFALSVINPLBLKAAPOTTEKISNWEGINDLA-STROYBLQL 60
KW				QY 121 EHHSDDHDHSEHENAAAGKNNKRNKALCPHDSSGCKDPDRSGKGSHPRBHASCRRNVD 180
KW				Db 121 EHHSDDHDHSEHENAAAGKNNKRNKALCPHDSSGCKDPDRSGKGSHPRBHASCRRNVD 180
KW				QY 121 EHHSDDHDHSEHENAAAGKNNKRNKALCPHDSSGCKDPDRSGKGSHPRBHASCRRNVD 180
KW				Db 121 EHHSDDHDHSEHENAAAGKNNKRNKALCPHDSSGCKDPDRSGKGSHPRBHASCRRNVD 180
KW				QY 181 NESVSPPRKGFMSRNTNENPQECFNASKLTSHGMGLOVPLNATEFNYCPLATINQIDA 300
KW				Db 181 NESVSPPRKGFMSRNTNENPQECFNASKLTSHGMGLOVPLNATEFNYCPLATINQIDA 300
KW				QY 181 NESVSPPRKGFMSRNTNENPQECFNASKLTSHGMGLOVPLNATEFNYCPLATINQIDA 300
KW				Db 181 NESVSPPRKGFMSRNTNENPQECFNASKLTSHGMGLOVPLNATEFNYCPLATINQIDA 300
OS				QY 241 IVALAVGTLSGDAFLHLDPHSHASHHHSHSHEPAMENKRGPLFSLHSSONIESATDS 420
XX				Db 241 IVALAVGTLSGDAFLHLDPHSHASHHHSHSHEPAMENKRGPLFSLHSSONIESATDS 420
PN	WO200255705-A2.			PA (CUDR) CUREGEN CORP.
XX	18-JUL-2002.			XX Mezes PS, Rastelli L, Herrmann JU, Macdougall JR, Zhong H;
PD				XX Caeman SJ, Shimkets RA, Gorman L, Crasta OR, Mysore KK;
XX	11-JAN-2002;	2002WO-US00609.		XX Folkers O, Boldog F, Eisens A, Spaderina SK, Vernet CAM, Bergh C;
PF				XX Spytte KA, Dipippo VA, Zerhusen BD, Peyman JA, Ellerman K;
XX				XX Stone DJ, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK;
PR	11-JAN-2001;	2001US-261013P.		XX Burgess CE, Edinger S;
PR	11-JAN-2001;	2001US-261014P.		XX
PR	11-JAN-2001;	2001US-261018P.		
PR	11-JAN-2001;	2001US-261026P.		
PR	11-JAN-2001;	2001US-261029P.		
PR	17-AUG-2001;	2001US-31170P.		
PR	10-SEP-2001;	2001US-31410P.		
XX				
PA				

QY	121	EHRSDHDHSHNHEAASGKUKRKAICPDEDSSGKDPRNSQGAHRDPHASSRRNVD	180
Db	121	EHSSD-----INHAASGKUKRKAICPDEDSSGKDPRNSQGAHRDPHASSRRNVD	174
QY	181	SVSASEVTSTVNTYSEGTHFLETETPRPGKLFPKDVSSTSPPSYTSKRSYSLAGRK	240
Db	175	SVSASEVTSTVNTVSGTHELETTETPRPGKLFPKDVSSTSPPSYTSKRSYSLAGRK	234
QY	241	NESYSEPRKGEMYSRNTNENPQECFNASKLISHGNGIQYPLNATEFENYLCPATINQIDA	300
Db	235	NESYSEPRKGEMYSRNTNENPQECFNASKLISHGNGIQYPLNATEFENYLCPATINQIDA	294
QY	301	RSCLJHTSEKKAIKPRTKTYSIQIAWGGPTAISIISPLSLIGVILVPLMNRVFKFLSF	360
Db	295	RSCLJHTSEKKAIKPRTKTYSIQIAWGGPTAISIISPLSLIGVILVPLMNRVFKFLSF	354
QY	361	LVALAVGFLSGDAFLHILLPHSAASHHSHEPMEMKRGPLFSELSSONTESAYEDS	420
Db	355	LVALAVGFLSGDAFLHILLPHSAASHHSHEPMEMKRGPLFHLSSQNTIESAYEDS	414
QY	421	TWKGLTALGGLYFMELVEHYLTLLIKQFDKKKKNQKPENDDVIEKKLKSXFSQSLSTN	480
Db	415	TWKGLTALGGLYFMELVEHYLTLLIKQFDKKKKNQKPENDDVIEKKLKSXFSQSLSTN	474
QY	481	BEKYDFTDORTGYLRADSQEPSPHDSCQPAVLEEEYTMIAHPQEVNEYPRGCKNKC	540
Db	475	BEKYDFTDORTGYLRADSQEPSPHDSCQPAVLEEEYTMIAHPQEVNEYPRGCKNKC	534
QY	541	HSEFHDTLGQSDDLIHHHDYHHLHHHHHEPHSHSORYSRDELKDAGVATLANNVI	600
Db	535	HSEFHDTLGQSDDLIHHHDYHHLHHHHHEPHSHSORYSRDELKDAGVATLANNVI	594
QY	601	MGDGLHNSFDGIALGAAFTEGLSSGLSTSVAEYCHELPHELGDFAVLIKAGMTVKQAVLY	660
Db	595	MGDGLHNSFDGIALGAAFTEGLSSGLSTSVAEYCHELPHELGDFAVLIKAGMTVKQAVLY	654
QY	661	NALSAMIALYLGATGFGIGHYAENWSMIFALTAGLFMYVALDVKPEMLHNDASDGCS	720
Db	655	NALSAMIALYLGATGFGIGHYAENWSMIFALTAGLFMYVALDVKPEMLHNDASDGCS	714
QY	721	RWGFFFLQNAGMILGFIMILLISIFEHKIVF	751
Db	715	RWGFFFLQNAGMILGFIMILLISIFEHKIVF	745
RESULT 10			
ID	ABJ37050	standard; Protein; 752 AA.	
XX			
AC	ABJ37050;		
XX			
DT	01-MAY-2003	(first entry)	
XX			
DE	Human breast cancer / ovarian cancer related protein #26.		
XX			
KW	Human; cyostatic; breast cancer; ovarian cancer.		
OS	Homo sapiens.		
XX			
PN	W02003000012-A2.		
XX			
PD	03-JAN-2003.		
XX			
PF	21-JUN-2002; 2002WO-US19773.		
XX			
PR	21-JUN-2001; 2001US-300159P.		
PR	27-JUN-2001; 2001US-301351P.		
XX			
PA	(MILL-) MILLENIUM PHARM INC.		
XX			
PI	Veiby OP;		
XX			
DR	WPI; 2003-267848/26.		

DIR	N-PSDB;	ABT31919
XX	Determining the F	
PFT	using specific P	
XX	CC	
SQ	Disclosure; Page	
XX	The invention con-	
CC	CC affiliated with br-	
CC	use of specific F	
CC	detection and tre-	
CC	sequences ABJ3702	
CC	related proteins.	
XX	Sequence 752 AA	
SQ		
	Query Match	
	Best Local Similarity	
	Matches 736; Conseqe-	
Qy	1 MARKLSTV	
Db	1 MARKLSTV	
Qy	61 FYRYGEENN	
Db	61 FYRYGEENN	
Qy	121 EHHSDDHH	
Db	121 EHHSDDHH	
Qy	181 SVSASEVTT	
Db	175 SVSASEVTT	
Qy	241 NESVSEPR	
Db	235 NESVSEPR	
Qy	301 RSCLIKPS	
Db	295 RSCLIKRS	
Qy	361 LVALAVGT	
Db	355 LVALAVGT	
Qy	421 TWKGLTAL	
Db	415 TWKGLTAL	
Qy	481 EERKVDTDD	
Db	475 EERKVDTDD	
Qy	541 HSHFHDTL	
Db	535 HSHFHDTL	
Qy	601 MGDGHLHNFE	
Db	595 MGDGHLHNFE	
Qy	661 NALSAMIA	
Db	655 NALSAMIA	
Qy	721 RWGYFFELQ	
Db	715 RWGYFFELQ	

PS Claim 11; Page 533-535; 607pp; English.

XX AF91658-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode.

CC AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

XX Sequence 831 AA;

Query Match 33.2%; Score 1337; DB 22; Length 831;

Best Local Similarity 35.5%; Pred. No. 2e-116; Gaps 26;

Matches 317; Conservative 131; Mismatches 241; Indels 204;

QY 1 MARKLSVILUTPASVTNPFLHEKAAFPOTTEK-----ISPWNWESGINVNDLAISTR 53
 5 MHTKFLCILCLTFFHHGNHCHE-EEDHGEAELFRHQGMTELP---SKFSKOAAENEK 60

QY 54 QYHQLQFLYNGENINSVYEGPRKLQNLIGTKRKRHLHD--EDH--HSD---- 101
 Db 61 KYYIEELFEYGGNLRGSEFFGLKLTNGIIGEKKVEINHEDGDHVSHLDLAYQEG 120
 Qy 102 --HEHHSDEHEHSDH 126
 Db 121 KHFHSHNFOQSHHNHNSENOTVTSVTKRNHKCDPEKETVEVSVDKFMEDHNNHLRH 180
 QY 127 DH-----HSHHNHAAS-----CKNKRKALCP 147
 Db 181 HERLHHFLDANNTHFHENDSTPPSERGEPSNEPSTEINNKTOEQSYKLPKGKRGKGS 240

QY 148 DHSD--SSGKDPRNSQK-----GHRPHEASGRNVYKDSASSEVTSTVNTYSEGT 200
 Db 241 NPNSEVATPDPFPHQDQEQQYEHNRVKHPDR-----RETRKREAPHKNNAILSLRK 326

QY 250 GRMYSRNTNENPQECFNASKLTSHGNGIQVPLATEENYLCPAINQIDARSCLHTSE 309
 Db 327 DL---NEDDHMHHECLNTQLYKYGHGANSPISTDLYTLCPLALYQIDSRLCIEHDK 382

QY 310 KKAELPPKTYSL-----QIAWYGGFAISIISLSESLGSLGTYLPLMRVFEKFLLSF 360
 Db 383 LIVEDINKDNLVPDEDEANIGASAWCAGISITVSLSLGGTYLPTINGQCKFLITF 442

QY 361 LYVLAYGTLSDFALLPLPHASHASHSHSHEEPDAMENKRGPLFHSISSIONIESAFDS 420
 Db 443 LYVLAYGTMSEDALLLPLPHSQGGHDHSQHHAH---GHHSHGHSNEKFLEE--YDA 494

QY 421 TWKGLTALLGGYFMEVLVHEVHTLIKQPKDKKKKNOK--KPENDDDVKEKKOLSKYESQIS 478
 Db 495 VLKGIVVALGGYLPLPIIECIRAFKHYKQQRGK-QKWMKMQNTEESTIGRKLSDHKLANT 553

QY 479 TNPEKVD----TDRTEGYLRADESEPFEDSCQPA---VLEEEYAHIAHAPDY 527
 Db 554 PSDWLQKPLLAGIDDSSVSEDRNLNETELDQEQSPPKNYLCIEEKIDISHSDGL 613

QY 528 YNEYVPRGCKNMKCHSHFHDYTLGOSDDLIHHHHYHHLHHONHPPHSHSQR--YSR 584
 Db 614 RT-----IHEHLHLAAH--NHHGENKTVRKHNHSHOPCAG 658

QY 585 EELKAGVATLAWVYVINGLHNFSQGLAIAAEGTSSGGLSTSVAFCHELPEHLGF 644
 Db 659 SDHKETGIANIAWVYTMGDIHNFSDGLAICAAFFAGIAGGISTSIAVFCHELPEHLGF 718

QY 645 AVLKGAGMTYQAVLYNALSAMAYLGOMATSILGHYAVNSWNIWATAGLTCYAVQANIGNLIGTAYQANITLWIFATAGMELYALND 778
 Db 719 AVLKGAGMTYQAVYNNLSAMMAYGNLIGTAYQANITLWIFATAGMELYALND 778

QY 705 MPEMLINDA--SDIGCSWGYFLQDAGMLGFQMLLISPEHKTVFRINF 755
 Db 779 MLEFMLQGDNEERFCPYGQFLQNLGLFGRAIMVIALXEDKVPDIFQ 831

Search completed: September 12, 2003, 22:14:03
 Job time : 78 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 12, 2003, 22:13:01 ; Search time 40 Seconds

Title: US-09-642-034-5
Perfect score: 4024
Sequence: 1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755

Scoring table: BIOSDM62
Gapop 10.0 , Gapext 0.5
Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-76:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3902	LIV-1 protein - hu	752	2	G02273		LIV-1 protein - hu
2	616	hypothetical prote	529	2	T0884		hypothetical prote
3	393.5	hypothetical prote	515	2	T2089		hypothetical prote
4	391	hypothetical prote	360	2	T1985		hypothetical prote
5	381.5	hypothetical prote	586	2	T2435		hypothetical prote
6	376	hypothetical prote	404	2	T25120		hypothetical prote
7	325	MIC_H-2Kt-w5-link	8.1	436	2	I49714	probable membrane
8	299	probable membrane	7.4	346	2	S49939	probable membrane
9	271.5	hypothetical prote	6.7	453	2	T3940	hypothetical prote
10	250.5	hypothetical prote	6.2	450	2	C96704	unknown protein, 2
11	208	hypothetical prote	5.2	338	2	B89325	protein C14H10.1 [
12	208	hypothetical prote	5.2	362	2	T1985	hypothetical prote
13	194.5	hypothetical prote	4.8	735	2	T4059	hypothetical prote
14	180	hypothetical prote	4.5	3119	2	T1814	protein g377 - mal
15	178	hypothetical prote	4.4	144	2	C44663	tryphozoite antigen
16	171.5	hypothetical prote	4.3	668	2	A44663	tryphozoite antigen
17	168.5	hypothetical prote	4.2	764	2	H71607	hypothetical prote
18	168	hypothetical prote	4.2	351	1	KGZQHL	histidine-rich pro
19	166.5	hypothetical prote	4.1	269	1	H71607	gufA protein homolog
20	163	hypothetical prote	4.1	65	2	D44663	tryphozoite antigen
21	163	hypothetical prote	4.1	283	2	C85838	hypothetical prote
22	161.5	hypothetical prote	4.0	972	2	S35583	DNA topoisomerase
23	160.5	hypothetical prote	4.0	477	2	T29592	hypothetical prote
24	158	hypothetical prote	3.9	140	2	A54223	histidine-rich pro
25	157	hypothetical prote	3.9	257	2	AH1665	hypothetical prote
26	155	hypothetical prote	3.9	279	2	H90592	hypothetical prote
27	155	hypothetical prote	3.9	295	2	T15544	hypothetical prote
28	155	hypothetical prote	3.9	330	2	D90548	hypothetical prote
29	154.5	hypothetical prote	3.8	96	2	A44571	hypothetical prote

ALIGNMENTS

30	154.5	hypothetical prote	3.8	1225	2	T16346
31	154.5	DNA-directed RNA p	3.8	2910	2	T28156
32	154	adhesin homolog HI	3.8	337	1	D61049
33	152	gufa protein homol	3.8	259	1	A69162
34	147.5	probable integral	3.7	291	2	F81444
35	146.5	hypothetical prote	3.6	905	2	AC2680
36	146.5	hypothetical prote	3.6	916	2	A97462
37	146	female-specific do	3.6	427	2	A33372
38	146	male-specific dou	3.6	549	2	B32372
39	146	hypothetical prote	3.6	1510	2	T33100
40	146	hypothetical prote	3.6	1785	2	T21558
41	146	hypothetical prote	3.6	1929	2	T21559
42	145.5	probable Fe(II) tr	3.6	348	2	T03385
43	145	Myx	3.6	254	1	S33876
44	143.5	zinc transporter 2	3.6	355	2	T5183
45	143	HRPII protein - ma	3.6	327	2	S31781

RESULT 1						
GO2273	LIV-1 protein - human	C;Species: Homo sapiens (man)	C;Date: 21-Dec-1996	#sequence_revision 06-Jun-1997	#text_change 05-Nov-1999	
		C;Accession: G02273	R;Green, C.; Gilhooly, E.M.; Walker, N.J.	submitted to the EMBL Data Library, November 1995		
		A;Reference number: H00961	A;Accession: G0273			
		A;Status: Preliminary; translated from GB/EMBL/DBJ	A;Molecule type: mRNA			
		A;Residues: 1-752 <RE>	A;Cross-references: EMBL:U41060; PIDN:AAA96258..1; PID:q1256001			
		C;Genetics:	A;Gene: LIV-1			

Query	MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;	97.0%	Score 3902;	DB 2;	Length 752;	
Best Local Simililarity	99.28;	Pred. No. 2.6e-27;				
Matches	736;	Conservative	0;	Mismatches	0;	Indels 6; Gaps 1;
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
Db	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
QY	1 MARKLSSVILLIIFALSVTNP.....FIMMLISFEHKIVFRINE 755;					
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Db	1 MARKLSSVILLIIFALSV					

QY	EEKVDTDDREGYLRAQSQEPHFDSSQPAVLEERVMIAHPQEVTNYVPKGCKNKC	540	Db	LLVEDINKDKNLVPEDEANTGASAWICGLISITVISLSSLGVTLVPLINQGOFKFLTF	442
Db	EEKVDTDDREGYLRAQSQEPHFDSSQPAVLEEFVIAHHHQEVNEYVPKGCKNKC	534	QY	LVALAVGTLISGDAELHLIPLPHSHASHHHHSHEPAPMEMKRGPLFSLSSHQNIEESEAFDS	420
QY	RSHFHPTLGSSDLDLHHHDYHILHHHHHPSHHSORYSREELKDAGVATLAWNVI	600	Db	443 LVALAVGTMISGDAELHLIPLPHSGGGHDHHQHHH-----GHGHSHGHESNKFLBE--YDA	494
Db	RSHFHPTLGSSDLDLHHHDYHILHHHHHPSHHSORYSREELKDAGVATLAWNVI	594	QY	421 TWKGLTALGGXFMELYEHVTLIKQFDKDKKKNQ	455
QY	MGDGLINFSDGLAIGAACTEGGLSSGISTSSTAVFCHELFHELDFAVLLKGMTYKQAVLY	660	Db	495 VLKGIVAVAGTIVLFLIECHTRMPKHYKOONKKK	529
Db	MGDGLINFSDGLAIGAACTEGGLSSGISTSSTAVFCHELFHELDFAVLLKGMTYKQAVLY	654	RESULT 3		
QY	NALSAMIALYGMATGIFIGHYAENYSMWIALTNGLEMYVALDVMPPEMLHNDAASDFCCS	720	T23089	hypothetical protein H13N06.5 - Caenorhabditis elegans	
Db	NALSAMIALYGMATGIFIGHYAENYSMWIALTNGLEMYVALDVMPPEMLHNDAASDFCCS	714	C;Species: Caenorhabditis elegans		
QY	RWGYFFLQNAGMILGFGINLLI	742	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000		
Db	RWGYFFLQNAGMILGFGINLLI	736	R;Lennard, N.		
Db	RWGYFFLQNAGMILGFGINLLI	736	submitted to the EMBL Data Library, October 1997		
			A;Reference number: Z19673		
			A;Accession: T23089		
			A;Status: preliminary; translated from GB/EMBL/DBJ		
			A;Molecule type: DNA		
			A;Residues: 1-515 <WIL>		
			A;Cross-references: EMBL:299942; PIDN:CA:17070.1; GSPDB:GN00028; CESP:H13N06.5		
			A;Experimental source: clone H13N06		
			C;Genetics:		
			A;Gene: CESP:H13N06.5		
			A;Map Position: X		
			A;Introns: 118/1; 156/2; 182/2; 306/1		
			Query Match 9.8%; Score 393.5; DB 2; Length 515;		
			Best Local Similarity 20.4%; Pred. No. 6.8e-21;		
			Matches 139; Conservative 64; Mismatches 153; Indels 327; Gaps 19;		
			A;Introns: 118/1; 156/2; 182/2; 306/1		
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			Query Match 9.8%; Score 393.5; DB 2; Length 515;		
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			Best Local Similarity 20.4%; Pred. No. 6.8e-21;		
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			A;Introns: 118/1; 156/2; 182/2; 306/1		
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			Best Local Similarity 20.4%; Pred. No. 6.8e-21;		
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			A;Introns: 118/1; 156/2; 182/2; 306/1		
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			Matches 139; Conservative 64; Mismatches 153; Indels 327; Gaps 19;		
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			Matches 139; Conservative 64; Mismatches 153; Indels 327; Gaps 19;		
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A; Molecule type: DNA			
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A; Cross-references: EMBL:Z			
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Query Match			
Best Local Similarity			
Matches 120 - Conservat			
QY 286 ENYLCPAINQ			
: : :			
Db 63 KFYMLAALNFS			
QY 320 SQIAWGGFIA			
: :			
Db 123 F---WGIGPATI			
QY 380 HASHHHHHSHH			
: : :			
Db 179 QAF-----			
QY 440 VTLIKQFDKDKI			
: : : :			
Db 211 MQLTYEFRRRR			
QY 484 VDIDDRTEGYLR			
: : : : :			
Db 257 VSEPPPTITRLQ			
QY 536 CKNK----GHSI			
: : : :			
Db 317 FSTRRRYAVVSGG			
QY 572 -----			
Db 377 INVEEPKESYEM			
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: : : : :			
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A; Status: preliminary; tra			
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A; Residues: 1-404 <WIL>			
A; Cross-references: EMBL:Z			
A; Experimental source: clo			
C; Genetists:			

Qy	265 FNASKLTLTSHGMGIOVPLNATENYLCPATIINOARDARSCLHTSEKKAFIPPKTYSLQIA 324
Db	130 ----- AGIKHLD----- TVTLWAY 145
Qy	325 WVGFSIATISIISFLSILGVLYLP-MANVFFKELLSFLSIVLAVALAVGTLSGDAFLHLHHS- - 381
Db	146 ALGATVLISAAFEFLV-- ELIPTVENSPRHSLQLLQLSFASGGLGPAGFLPHIALE 202
Qy	382 -HASBH---- HSHBHEEPAMENKRGPIFPHLSSQNIEEAYEDSTKNGLALGGYFM 434
Db	203 PH-SHRAEQPKXGHES- - GQGRLLS----- VGLAWLSCGVYAF 238
Qy	67 HTSHR--EIQHSLSTIATKWWFSLVSLAVGFTPLM-NRVEKFPLLSFTA 363
Db	364 LAVPLGSDAFLHLPHSASHHHHSHEEPAMENKRGPIFPHLSSQNTEEAYEDSTWK 423
Qy	122 -GAGGLGDLALITPPLSPHDSDHDH----- RHHSHKEHDHDSNQLRV 170
Db	424 GLTAGLGYMFMEVHILITLKQFKKKKKNNQQKPPENDDVIEIKQLSKYESQLSTNEEK
Qy	171 GTFVAGLIVMFMEVYLRLIK-----
Db	484 VDTDDECTYLRADSOEFSHPSDQSOPAVLSEEYVMAAHPOEVINYYVRGCRKNKCHSH 543
Qy	193 -----
Db	544 FHDTLGQSDDLTHHHHDYHHLHHHHHHNPHSHSORYSR-EELKDAGYATLAWYTM 601
Qy	199 ----- HENGHTVADEHHHLNHDHSEKQOEGIJD-VKASAYILMV 242
Db	602 GDGLINNESDCGLAAGAATPEGLSSGCTSTSVAVECHELPHELGAVALKAGMTVKQAVYN 661
Qy	243 ADFVNNTDGLAISASPAAGNLGNNTTFLVLLHELPHEVGSFATLVQSFSKYQATRLQ 302
Qy	662 AISAMALAYLMGATGFIGHYA---ENVSNWIFIALTAGLFMVTALDMVDEMHNDA SDH 717
Db	303 AVTAGNIGCVSLLSNPDGLNNADTSAIMPFIAGGIFTAVSVNPFELL-ESSDH 360
Qy	718 G---CSRNGYFFLQNAGMLIGFGTMIL 741
Db	361 NNLSKVAKNEAQSLVHVAICMGVANNYI 388
RESULT 7	I49714
C;Species: Mus musculus (house mouse)	MHC H-2K/t-w5-1-linked ORF precursor - mouse
C;Accession: I49714	C;Title: A putative transmembrane protein with histidine-rich charge clusters encoded in
A;Status: preliminary; translated from GB/ERBL/DBJ	C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
A;Residues: 1-436 <RES>	A;Cross references: GB:M32010; NID:9193738; PID:AAA37767.1; PID:9309286
Query Match 8,1% Score 325; DB 2; Length 436;	Best Local Similarity 22.68; Pred. No. 5.5e-16;
Matches 135; Conservative 51; Mismatches 143; Indels 268; Gaps 24;	Indels 164; Gaps 10;
Qy	93 HDHDHDSHDE-HHSDHERHS--- HEHHSDEHHSDHDEHSH MNHAASGKAKRKA 145
Db	55 HIGHSGHSHDEFHGHGHTHEISIWHGHASHDHSHSREELIGHGSIGHS----- 104
Qy	946 CPDHDSGSRDKPRNSQKG-AERPHASGRNRYDSVSASEVTSVNTYSEGTHELET 204
Db	105 --HDSLHHLG---- -GHBGHHR-BPSHG----- 123
Qy	205 IETPRGKLPKDPDYSSPPSTSKRSVSLAGKTNVESVERPKGMWSRNNTNENQEC 264
Db	124 -----LSGVT----- -DVTMVGAIPLGFIS-FILL--- 147
Qy	449 DKKKNQKPKPENDDVTEIKQLSKYESQLSTNEEKVDTDDRTEGYIRADSQEPSHFDSQ 508
Db	148 DKTMLLSTSND----- 161
Qy	509 PAYLBEEVMIAHPOEVINYVPRGCKNCKISHFTLQSDDDLHHDYHILHH 568
Db	124 -----TSRAG----- 129

RESULT 13

Db 299 SSSLY-----PGYUNIFSDGVHNTFTD 319
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T19285
 R;White, S.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: T19102

Db 611 GLAIGAAF-TEGLISGLSTSVAYCFELPHELPFDAVLLKAGMTYKQAVLYNALSAMAY 669
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C;Accession: B88625
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes, development, behavior and disease. www.sanger.ac.uk/projects/c_elegans/
 A;Reference number: A75000; PMID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/sc/c_elegans and www.sanger.ac.uk/projects/c_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999, and
 A;Cross-references: B88625
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-338 <STO>
 A;Cross-references: GB:cnr_X; PIDN:CAA90736.1; PID:93874326; GSDB:GN00028; CESP:C14H10.1
 A;Gene: C14H10.1
 A;Map position: X

Query Match 5.2% Score 208 DB 2; Length 362;
 Best Local Similarity 19.9%; Pred. No. 1.4e-07; Indels 182; Gaps 13;
 Matches 81; Conservative 53; Mismatches 91; Gaps 13;

Qy 310 KKARIPPKTYSIQIAWGGFAIASIISFLSFLGIVLP---LMNRYPFKELLSFLVAL 364
 Db 100 KKGEVTSAT----WIALIGCSLVYSTGTILPAFLPANHYVLLSQQRNLILGF 153
 Qy 365 AVGTLSGDAFLPLPHASHSHSHHEPAMEKMRGPFLSHSSONTEASYFDSTWKG 424
 Db 154 AIGSLIADVFHLLEPEASNE----NHVSI----SKLASSEE 203
 Qy 425 LTALGGLYFMFLIVEHVLKLQPKDKKKKNOKKPENDDDVEIKQLSKYESQLSTNEKV 484
 Db 182 LCVLAG-YLTFL----SLI----SKLASSEE 203
 Qy 485 DTDDRTEYLRADSQEPSPHSDFSQOPAVLEEEYVNEVPRGCKNCHSHF 544
 Db 204 -----QHKASSAHF----LNAC----LNAC----217
 Qy 545 HDILGQSDDLTHHHHDYHHLHHHHQHNPHPHSQRSYREELKDAGYTLAWMYIMGDG 604
 Db 218 -----AYLNLFANIGD----LNAC----LNAC----228
 Qy 605 LHNFSGLAIGAIAFPTRGSSGLSTSVAWFCHELPFDAVLLKAGMTYKQAVLYNALS 664
 Db 229 -NFAHGLAVGSSFLYSTKGINTWITLHEPIDEFLRADFGKTNAILAQLT 286
 Qy 665 AMIAYLGMATGFIGHYAENVS-WIFALTAGLEMVYALDMVPM 709
 Db 287 AAFGYLGSLVALHL-HTSNVPVIETLIPFTAGGLNALTLLPEI 331
 R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burträger, B.; O'Callaghan, M.; Parsons, J.; Percy, P.; Hawkins, T.; Hillier, L.; Jier, M.; Saunders, D.

RESULT 14

Db 485 DTDDRTEYLRADSQEPSPHSDFSQOPAVLEEEYVNEVPRGCKNCHSHF 544
 C;Species: Caenorhabditis elegans
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T45059
 Qy 545 HDILGQSDDLTHHHHDYHHLHHHHQHNPHPHSQRSYREELKDAGYTLAWMYIMGDG 604
 Db 218 -----AYLNLFANIGD----LNAC----LNAC----228
 Qy 605 LHNFSGLAIGAIAFPTRGSSGLSTSVAWFCHELPFDAVLLKAGMTYKQAVLYNALS 664
 Db 229 -NFAHGLAVGSSFLYSTKGINTWITLHEPIDEFLRADFGKTNAILAQLT 286
 Qy 665 AMIAYLGMATGFIGHYAENVS-WIFALTAGLEMVYALDMVPM 709
 Db 287 AAFGYLGSLVALHL-HTSNVPVIETLIPFTAGGLNALTLLPEI 331
 R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burträger, B.; O'Callaghan, M.; Parsons, J.; Percy, P.; Hawkins, T.; Hillier, L.; Jier, M.; Saunders, D.

RESULT 15

Db 100 KKGEVTSAT----WIALIGCSLVYSTGTILPAFLPANHYVLLSQQRNLILGF 153
 C;Species: Caenorhabditis elegans
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T45059
 Qy 545 HDILGQSDDLTHHHHDYHHLHHHHQHNPHPHSQRSYREELKDAGYTLAWMYIMGDG 604
 Db 218 -----AYLNLFANIGD----LNAC----LNAC----228
 Qy 605 LHNFSGLAIGAIAFPTRGSSGLSTSVAWFCHELPFDAVLLKAGMTYKQAVLYNALS 664
 Db 229 -NFAHGLAVGSSFLYSTKGINTWITLHEPIDEFLRADFGKTNAILAQLT 286
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RESULT 12

T19285 hypothetical protein C14H10.1 - Caenorhabditis elegans

A: Note: Y39B6B, ag

Annotation: Y39B6B.agg

Result No.	Score	Query	Match	Length	DB ID	Description
1	455	11.3	449	1	CSUP_DROME	09r3a4 drosophila
2	393.5	9.8	515	1	KE4L_CAEEL	09rt97 caenorhabdi
3	389	9.7	476	1	KE4_MOUSE	Q31125 mus musculu
4	375.6	9.3	404	1	Y4JK_CAEEL	09r4uc4 caenorhabdi
5	355.5	8.8	469	1	KE4_HUMAN	092504 homo sapien
6	299	7.4	346	1	YIC3_YEAST	P04544 saccharomyces
7	282.5	7.0	352	1	KE4_BRARE	Q9paf8 brachydanio
8	273	6.8	355	1	Y816_DROME	Q9rafo drosophila
9	168	4.2	351	1	HRPX_PLATO	P04929 plasmidium
10	165	4.1	338	1	TARL_ARATH	Q9ub64 arabidopsis
11	161.5	4.0	972	1	TOP1_DROME	P30189 drosophila
12	157	3.9	302	1	HYPB_BRATA	Q42577 bradyrhizobium
13	154	3.8	337	1	ZNUA_HAEIN	P44526 haemophilus
14	147.5	3.7	291	1	ZUPT_CAME	Q9pnz2 campylobacter
15	146	3.6	549	1	DSX_DROME	P221023 drosophila
16	145	3.6	254	1	GUTA_MIXXA	Q00916 myxococcus
17	142	3.5	1709	1	CHDL_HUMAN	Q14646 homo sapien
18	141	3.5	950	1	URBL_UTSWA	Q43349 ustilago maydis
19	140	3.5	332	1	HRPL_PLAFA	P05327 plasmidium
20	140	3.5	732	1	YLH3_SCHPO	Q9hgq3 schizosaccharomyces
21	139.5	3.5	2026	1	CYAA_YEAST	P088778 saccharomyces
22	137.5	3.4	1711	1	CHDL_MOUSE	P40201 mus musculus
23	135.5	3.4	149	1	EGBS_SCHEMA	P08816 schistosoma
24	135	3.4	722	1	HMN2_DROME	P22808 drosophila
25	134	3.3	503	1	YKR5_YEAST	P34240 saccharomyces
26	134	3.3	1093	1	PI4K_DCDC1	P54677 dictyostelia
27	133	3.3	657	1	KNOB_PLAFN	P046719 plasmidium
28	131.5	3.3	1402	1	SALM_DROVI	P384806 drosophila
29	130.5	3.2	257	1	ZUPT_COLI	P24198 escherichia
30	129.5	3.2	626	1	DALY_DROME	Q21114 drosophila
31	129	3.2	257	1	ZUPT_SALTY	P09436 plasmidium
32	129	3.2	285	1	ZUPT_CLOPSE	P04930 plasmidium
33	127.5	3.2	390	1	PC_DROME	P21750 drosophila

Scoring table: BL05062
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127853

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Page 6

QY	516 EYMIAAHPQEYVNEYVPRGCKNKCHSHFHDTLGOSDDLIHHHHHDYHILHHHHQNHP	575	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	304 -----	303	CC the European Bioinformatics Institute. There are no restrictions on its
Db	576 HSHSQRYSREEFKDGAVTLLAWRIVMDGLNSLGAATGGISLGSLSGTYAVTCW	635	CC use by non-profit institutions as long as its content is in no way
QY	: : : : : : : : : : : : : : : : : : :	639	CC modified and this statement is not removed. Usage by and for commercial
Db	304 -----	339	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
Db	LAADFTHNFTDGLAAGASFLVGAVAYTTILH	339	CC or send an email to license@isb-sib.ch).
	-----	-----	CC
	-----	-----	CC
QY	636 ELPEIIGDFAVIL 648	648	DR EMBL; AE003771; AAC1195.1; ;
Db	: : : : : : : : : : : : : : : : : : :	340 EVFHEIGDFAVIL 352	DR FlyBase; FBgn039714; CG7816.
QY	Y816_DROME	STANDARD;	DR InterPro; IPR033659; Zn_transpt_Zip.
ID	Y816_DROME	PRT;	DR Pfam; PF02535; Zfp; 1.
AC	QVATO;	355 AA.	KW Hypothetical protein; Transmembrane; Glycoprotein.
DT	16-OCT-2001 (Rel. 4.0, Created)		FT TRANSMEM 37 57 POTENTIAL.
DT	16-OCT-2001 (Rel. 4.0, Last sequence update)		FT TRANSMEM 79 99 POTENTIAL.
DT	15-SEP-2003 (Rel. 4.2, Last annotation update)		FT TRANSMEM 118 138 POTENTIAL.
DE	Hypothetical protein CG7816.		FT TRANSMEM 273 293 POTENTIAL.
GN	Drosophila melanogaster (Fruit fly).		FT TRANSMEM 301 321 POTENTIAL.
OC	Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		FT CARBOYD 4 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		FT CARBOYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC	Ephydarioidea; Drosophilidae; Drosophila.		SQ SEQUENCE 355 AA; 38870 MW; 015270390741FF8 CRC64;
OX	CBI_TAXID=727;		Query Match 299 DARSCLIETSEKKAEPKPTYSLOTA-WYGGFTAISITISPLSLIGVLYPL--MNRFVF 354
RN	[1]		Best Local Similarity 20.8%; Pred. No. 6. 8e-12;
RP	SEQUENCE FROM N.A.		Matches 96; Conservative 76; Mismatches 162; Gaps 14;
RC	STRAIN=Berkeley;		Db 9 DEHTIMATYENLNLMQYMEYFSFEETPPWFFSLIGSVIGLSGIFPLIPLPTERMAEGY 68
RX	Medline=20190006; PubMed=10731132;		Db 355 K----FLLSFELVALAVGTLSGDAFLHLPLPHASHHHSHEPAPMEMKRGPLFSLHS 409
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		Db 69 KDPADSKLLRVLISFATVGLLGVDPLHLPEAEG---DNQDPS-----SHPSL 114
RA	Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,		QY 410 QNIESSAYFDSTWKGLALGGLYFNLWYHVTLIKOFDKKKNNQQKKEENDDDVETIKQ 469
RA	Ananatides P.G., Scherer S.E., Richards S., Asburyer M., Henderson S.N.,		Db 115 RS-----GLWLSQLGLIFTWKTFS-----
RA	George R.A., Lewis S.E., Richards S., Yandell M.D., Zhang Q., Chen L.X.,		QY 470 LSKYBSQLSTNEEKVDDTRTEGYLRSQEPSPHDSQDDTQFVLTPEYMAHHPQEVIN 529
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		Db 136 -----GYSADDENP-----QPKCVELANC1-LRKHGOLPE 166
RA	Brandon R.C., Rogers Y.-H.-C., Blizquez R.G., Champe M., Pfeiffer B.D.,		RA 530 EYVPRGCKNCKSHFHDTLQGSDDLIHHLHHHHQNHPHSHQSORYSREELKD 589
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,		Db 167 GETSESGGACDI---PBYGVKCFL-----
RA	Abril J.F., Agbavanyi A., An H.-J., Andrews Pannoch D., Baldwin D.,		Db 590 AGVATIAWATYNGDGLINFSGLAAGATTEGLSSGLTSVATEHELPEHDFEAULK 649
RA	Balilow R.M., Basu A., Bayendale K., Bayraktaroglu L., Beasley E.M.,		Db 201 QPKVYAGYLNLANSINFTGLAYASLPSFRGLATPAILHEIHEYDFATLLR 260
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brokstein P., Brottier P.,		QY 650 AGMT---VHQAVLYNALSAMAYLGMATGIFHYAENSNWFALTAEMLYVALDMY 706
RA	Botcharova D., Botchan M.R., Bouck J.J., Harris M.,		Db 261 SGFSRKAARQLITASAGLGLALVAGSGGSVTSAMARTSWIXPFTTAGFLHIALTVL 320
RA	Burtis K.C., Busam D.A., Butler H., Cadine E., Center A., Chandra I.,		QY 707 PEMLHNDA5DHGCSRWYEFFLQNAGMLGFQIMLIS-IEFH 747
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		Db 321 PDLLKEERKESIK----QLLAFLGITALMAMVMPLEFH 355
RA	de Pablo B., Deicher A., Deng A.D., Dew I., Dietz S.M.,		RESULT 9
RA	Dodson K., Doud I.E., Downes M., Dugan-Rocha S., Dunlop B.C., Dunn P.,		HRP_X-PLALO STANDARD; FRT; 351 AA.
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		ID HRP_X-PLALO STANDARD; FRT; 351 AA.
RA	Foster C., Gabriele A.E., Garg N.S., Gelbart W.M., Glässer K.,		AC P04929; DT 13-AUG-1987 (Rel. 05, Created)
RA	Gliodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,		DT 13-AUG-1987 (Rel. 05, Last sequence update)
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		DT 15-JUL-1999 (Rel. 38, Last annotation update)
RA	Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		DE Histidine-rich glycoprotein precursor.
RA	Jaijali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,		OS Plasmodium lophurae.
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		OC NCBI_TAXID=585;
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		OX [1]
RA	Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,		RN
RA	Mount S.M., Moy M., Murphy L., Munry D.M., Nelson D.L.,		RP SEQUENCE FROM N.A.
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paileb J.M.,		RX MEDLINE=85061608; PubMed=6095114;
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		RA Ravetch J.V., Feder R., Pavlovec A., Blobel G.;
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,		CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
RA	Shieh B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		CC -1- SIMILARITY: BELONGS TO THE KEF/CATSUP FAMILY.
RA	Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,		CC This SWISS-PROT entry is copyright. It is produced through a collaboration
RA	Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zhang X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RA	"The genome sequence of Drosophila melanogaster."		
RA	Science 287:2185-2195(2000).		
CC	-1-		
CC	SEQUENCE FROM N.A.		
CC	RP MEDLINE=85061608; PubMed=6095114;		
RA	Ravetch J.V., Feder R., Pavlovec A., Blobel G.;		

RT	"Primary structure and genomic organization of the histidine-rich
RT	protein of the malaria parasite Plasmodium leghumae.";
RJ	Nature 312:615-620(1994)
-1	MISCELLANEOUS: IN THE INTRABRTHROCYTIC STAGES OF DEVELOPMENT OF P. LOPHURAE IN DUCKS, THERE IS A SYNTHESIS OF A MAJOR PROTEIN THAT ACCUMULATES TO COMprise AT LEAST 50% OF THE CELLULAR MASS: THE HISTIDINE RICH PROTEIN.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstations in Europe. Non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL: X01460; CAA25698.1; -.
CC	PIR: A22692; KZQHL.
CC	KW Malaria; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 23	
FT PROPEP 24 47	HISTIDINE-RICH GLYCOPROTEIN.
FT CHAIN 48 351	N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 40 40	2 X 16 AA TANDEM REPEATS.
FT DOMAIN 59 90	
FT REPEAT 59 74	16-1.
FT REPEAT 75 90	16-2.
FT DOMAIN 91 123	2 X 17 AA TANDEM REPEATS.
FT REPEAT 91 107	17-1.
FT REPEAT 108 123	17-2.
FT DOMAIN 124 153	2 X 15 AA TANDEM REPEATS.
FT REPEAT 124 138	15-1.
FT REPEAT 139 153	15-2.
FT DOMAIN 173 351	18 X 10 AA TANDEM REPEATS.
SEQUENCE 351 AA; 44032 MW; D19A8D47D890453 CRC64;	
Query Match 4.2%; Score 168; DB 1; Length 351;	
Best Local Similarity 13.3%; Pred. No. 0.00015;	
Matches 72; Conservative 30; Mismatches 116; Indels 322; Gap 0	
Qy 63 RYGENANSLSYEGFRKLLQ--NIEGDK----IKRILTHHDADSDHEBHS-DHEE	
Db 19 Q1SGSNCSCLSSLYKIPQTGSNTIDFRLVEDTYVPEFHHEHKHHPEEHPEHPEH	
Qy 113 DHE----HSDHEIHHSDHDHSHHHNHAASGKKNRKALCPDHDSKQDPRNNSQO	
Db 79 HHPEHHHEPHHEEEHHHHPHPHHHHH-----PPHHHHHLGHH-----	
Qy 166 AHREPHASGRNKKVSYSASEYTSTVNTYSESEGTHLETFPRPGKLFKDYSSTS	
Db 119 -HHHHAAHHHHHE-----HHHHAAAH-----	
Db 226 VTSKRSVSLAGRKTNESYSEPRKGFMYSRNTNNPQECFNASKLLTSHGMGIQVPL	
Db 79 HHEEEHHHHHHAAAHHEPVPHHHGGYH-----	
Qy 286 EPNYLCPAINQIDRSCLHTSEKIEPKTKYSLQ-TAWVGGFATIISITFSLLG	
Db 170 -----	
Qy 346 VPMLNRYEFKKLSSLVALAVGTLSGDAFLHLLPHASHHHHSHEEPAMEMKGPR	
Db 170 -----	
Qy 406 HLSSQNLEESAYEDDTWKGLTAIGGYFMEVLTILIKQFDKKKKNNQQKKPNDDD	
Db 185 -----	
Qy 466 IKKQLSYESLSTMEEKYDTRTEYLRAQSOPSHPSOCAPVIEEPMVLAH	
Db 185 -----	
Qy 526 EYNEYVPRGCKNKCHSHFHDTLGOSDDLTHHHDYHTLHHHEHHONHPPHSQSRY	
Db 185 -----	

DR	M74557; AAA28951.1;	-.	DT	15-SEP-2003 (Rel. 42, Last annotation update)
DR	U80064; AAC24138.1;	-.	DE	Hydrogenase nickel incorporation protein hyPB.
DR	AEO03438; AAF4440.1;	-.	GN	HYPB OR BLI6931.
DR	PTR: S3521; S3521.	-.	OS	Bradyrhizobium japonicum.
DR	HSSP; P11387; 1A35.	-.	OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
DR	FLYBase; FBgn004924; Top1.	-.	OC	Bradyrhizobiaceae; Bradyrhizobium.
DR	GO; GO:0005777; C: cytoplasm; IDA.	-.	NCBI_TAXID	375;
DR	GO; GO:0005634; C:nucleus; IDA.	-.	OX	
DR	GO; GO:0009735; P: embryonic morphogenesis; IMP.	-.	RN	SEQUENCE FROM N.A.
DR	GO; GO:0002168; P: larval development (sensu Insecta); IMP.	-.	RC	STRAIN=USDA 110.
DR	GO; GO:0002202; P: oogenesis; IMP.	-.	RX	MEDLINE=9413773; PubMed=8305450;
DR	Interpro; IPRO01631; Topoisomerase_I.	-.	FU	C., Maier R.J.;
DR	PFam; PF02919; Topoisomerase_I_N.	1.	RT	"Nucleotide sequences of two hydrogenase-related genes (hyPA and hyPB) from Bradyrhizobium japonicum, one of which (hyPB) encodes an extremely histidine-rich region and guanine nucleotide-binding domains."
DR	PFam; PF01028; Topoisomerase_I.	1.	RT	
DR	PRINTS; PR00416; BUTPISMASEI.	-.	RT	
DR	SMART; SM00435; TOPOE; 1.	-.	RT	
DR	PROSITE; PS00176; TOPOISOMERASE_I_EUK; 1.	-.	RT	
KW	Isomerase; topoisomerase; DNA-binding.	-.	RT	Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
FT DOMAIN	32	39	RL	DNA Res. 9:189-197(2002).
FT DOMAIN	40	198	RP	-!- FUNCTION: MN WORK IN THE MOBILIZATION OF NICKEL INTO HYDROGENASE
FT ACT_SITE	930	930	RP	CC ENZYME: BINDS 9 NICKEL IONS PER MOLECULE.
FT ACT_SITE	40	40	RP	-!- SIMILARITY: BELONGS TO THE HYP/HUPM FAMILY
FT CONFLICT	40	40	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT CONFLICT	46	46	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
FT CONFLICT	201	201	CC	the European Bioinformatics Institute. There are no restrictions on its
SEQUENCE	972 AA;	111688 MW;	CC	use by non-profit institutions as long as its content is in no way
			CC	modified and this statement is not removed. Usage by and for commercial
			CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Query Match	4.0%	Score 161.5; DB 1; Length 972;	CC	
Best Local Similarity	19.7%	Prep. No. 0_0017;	CC	
Matches 103; Conservative 79; Mismatches 162; Indels 179; Gaps 22;	CC			
QY	68 NSLSYE--GFRKLLOQIGDIDKIKRTHHDHSDHEHSDEHHS-DHEHHS 124	-.	DR	EMBL: L24513; APA17763.1; -.
Db	9 NSIHTQNSCCEVQNSGV--TTNGHHH-HHHHSSSSSKHSSSSDKHRDRERHS 65	-.	DR	EMBL: AP005260; BAC52196.1; -.
QY	125 DHDHHHHNHAASGKNRKAKLCPDDSDSSG----KDPRNSSQGKAHRPEHASGRNVK 179	-.	DR	InterPro; IPR004392; HYPB.
Db	66 SNSSSSKEHKSSSRDRDR----HKSSSSSKHRDDKDERGDSNSHRSGSSSHDK-K 119	-.	DR	InterPro; IPR003894; HYPB_Ureg.
QY	180 DSVSSEVSTVNTVSEGTHFLEETIPRPGKLTPKDVSSST--PPVYTSKRSVSLAG 237	-.	DR	Pfam; PF01455; HYPB_Ureg.1.
Db	120 DGSSSSKHKs----SSGHHKRKKDKKERDKDKDGGSSSSSRDKERSSS 173	-.	DR	TIGRFAMs; TIGR00073; HYPB; 1.
QY	238 RKTNEVSSEPRGEMYSRNTNNPQEFCNASKLTSIHMGTQVPLNATEFNYLCPALINQ 297	-.	KW	Metal-binding; Nickel; Complete proteome.
Db	174 HKSSSSSSSKKHSSSSRHSSSS 196	-.	FT	DR DOMAIN 16 54 HHS-RICH.
QY	298 IDARSCLHTSEKKAETPPKTVSLOIAYGGFTAISLSP-LSLIGVILVPLMNRYFFKF 356	-.	FT	CONFFLICT 72 72 A > T (IN REF. 1).
Db	197 ---SKDIPSPSTGDGVPKPEVSQLMHG----SDAFQMQQLG----- 233	-.	SQ	SEQUENCE 302 AA; 32708 MW; D3B554F24AB90AA CRC64;
QY	357 LLSPFLVALAVTGILSGDAFLHLPLASHASHSHSPAMEMKRSPFLPSHLSSONLEESA 416	-.	Qy	92 IHHDHDSHSDHEHSDHEHSDHEHSDHEHSHDHSHHHNHAAS---
Db	234 --SYAAAAGTNTENG-----NVAAGANYKNGYESIVDIKK---EEESPNNLSSOAS 280	-.	Db	14 IEAHDDHHDDGHDDH---GHDGHHHHHGDODHHHDDHAGLDGJGDNPAQO 69
QY	417 YFDSTWKGLTAJGGLFM-----FLVEHYLTIIKQ----- 446	-.	Qy	138 -----GKNRKALCPDH-----DSDSGKDPRNSQK 164
Db	281 SCD-----1SMSQRADEPPVVKHQEQSYAEEDSTMNNDHDAEHDDE 328	-.	Db	70 KIAGMSSDRITQVERDILGKNDR-LAADNRFARFADEVLAFLNLYSSPAGKTSLLVRAV 127
QY	447 ----FKDKKKKKQKRP---ENDDDEVIK-----KOLSKYESOLSTNEEKVD 485	-.	Qy	165 GAIRPEIASG-----RENVIDSVASETIVNTVEGTIF-----LETEIPR 209
Db	329 DVPLAMRKERQETDRDGMDNDDDIPLIARKKKTKKESKRSKRVKEEPSD 388	-.	Db	128 SELKDSAAIGVIEGQDQTSNDAERIRATGVPQVNT-GKGCHLDAANVGYDELPLWN 186
QY	486 TDDREGILRADSQEPHSQDSQQAV-----LEEREV 517	-.	Qy	210 PGKLFPKDVSSSTPPSVTSKRSVSLAGRKTNESSEPRKGEMYSRNTNNPQECAFASK 269
Db	389 DGYNVKPKKKMKKEP-----EPAVSPGSKRQAKAKVEEEEV 425	-.	Db	187 GGLLFINVGIVPLNATEFNLYCPAFTGEACKTYFESTGEDKPK-----YPMFAASS 235
RESULT 12			Qy	270 LATSRRGNGIQVPLNATEFNLYCPAFTGEACKTYFESTGEDKPK-----LIRTSEKKAIEPPKTYSLQI -- 323
HYP_BRAJA	STANDARD;	PRT;	Db	
ID	HYP_BRAJA		AC	
AC	Q45257;		DT	
DT	01-NOV-1997 (Rel. 35, Created)		DT	
DT	28-FEB-2003 (Rel. 41, Last sequence update)			

Page 13

Search completed: September 12, 2003, 22:14:45

Q8nc35	homo sapien	17	596	14.8	160	4	Q8BZ35
091v10	mus musculus	18	586.5	14.6	462	11	Q9W1W0
Q9c0K1	homo sapien	19	583	14.5	460	4	Q9c0K1
Q9d54	mus musculus	20	581.5	14.5	462	11	QD5V4
Q9d126	mus musculus	21	580.5	14.4	462	11	QD426
Q96bb3	homo sapien	22	579	14.4	481	4	Q96bb3
Q9vui9	drosophila	23	575.5	14.3	519	5	Q9vui9
Q8bbcg3	mus musculus	24	573.5	14.3	462	11	Q8bbcg3
Q96sm9	homo sapien	25	573	14.2	393	4	Q96sm9
Q9d479	mus musculus	26	552	13.7	660	11	QDAT9
Q95ka5	macaca fasciata	27	551	13.7	654	6	Q95ka5
Q96ne4	homo sapien	28	545.5	13.6	654	4	Q96ne4
Q9h6t8	homo sapien	29	543.5	13.5	647	4	Q9h6t8
Q9nxcl4	homo sapien	30	404	10.0	626	4	Q9nxcl4
Q8ch14	mus musculus	31	396.5	9.9	230	11	Q8ch14
Q9xvr4	caenorhabditis elegans	32	391	9.7	360	5	Q9xvr4
Q9nxz2	homo sapien	33	390.5	9.7	149	4	Q9nxz2
Q22395	caenorhabditis elegans	34	382	9.5	512	5	Q22395
Q81490	caenorhabditis elegans	35	374.5	9.3	505	5	Q81490
Q9n354	caenorhabditis elegans	36	358.5	8.9	157	5	Q9n354
Q8h9f6	arabidopsis thaliana	37	355	8.8	468	10	Q8h9f6
Q96mi3	homo sapien	38	327.5	8.1	129	4	Q96mi3
Q96lf0	homo sapien	39	321	8.0	368	4	Q96lf0
Q8xxx9	ratstomia sativus	40	299	7.4	268	16	Q8xxx9
Q9nsa4	homo sapien	41	290	7.2	125	4	Q9nsa4
Q8aw42	brachydoracites	42	285	7.1	348	13	Q8aw42
Q9ut11	schizosaccharomyces pombe	43	271.5	6.7	453	3	Q9ut11
Q81l42	plasmoidium falciparum	44	246	6.1	384	5	Q81l42
Q96hf2	homo sapien	45	234.5	5.8	388	4	Q96hf2
ALIGNMENTS							
RESULT 1							
Q13433	homo sapien	Q13433	Q13433	PRELIMINARY;	PRT;	749	AA.
AC		Q13433;	Q13433;				
DT	01-NOV-1996	(TREMBLel.	01,	Created)			
DT	01-JUN-2001	(TREMBLel.	17,	Last sequence update)			
DT	01-MAR-2003	(TREMBLel.	23,	Last annotation update)			
DB				Estrogen regulated LIV-1 protein.			
GN	LIV-1.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OC	NCBL-TaxID:9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Green C., Morgan H.						
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.						
DR	EMBL: U41060; AAA9658.; -.						
DR	InterPro: IPR003689; Zn_transpt_Zip.						
DR	Pfam: PF0235; Zip; 1_						
SQ	SEQUENCE	749 AA;					
SUMMARIES							
SUMMARY							
No.	Score	Query Match	Length	DB ID	Description		
1	396.9	98.6	749	4 Q13433	Q13433 homo sapien		
2	353.2	88.0	765	11 Q8c145	Q8c145 mus musculus		
3	253.5	63.0	505	11 Q85118	Q85118 mus musculus		
4	228.0	56.7	433	4 Q8lxr3	Q8lxr3 homo sapien		
5	205.7	51.1	382	4 Q96ip5	Q96ip5 homo sapien		
6	133.7	33.2	835	4 Q9uef5	Q9uef5 homo sapien		
7	90.2	22.4	381	11 Q8bx42	Q8bx42 mus musculus		
8	787.5	19.6	701	5 Q9vsl7	Q9vsl7 drosophila		
9	73.4	18.2	528	6 Q9gv2	Q9gv2 macaca fasciata		
10	70.3	17.5	228	11 Q8c012	Q8c012 mus musculus		
11	657.5	16.3	539	4 Q8ny3	Q8ny3 homo sapien		
12	652.5	16.2	535	11 Q9db56	Q9db56 mus musculus		
13	652.5	16.2	535	11 Q9d09	Q9d09 mus musculus		
14	640	15.9	489	11 Q8ydl0	Q8ydl0 mus musculus		
15	63.7	15.7	531	4 Q1543	Q1543 homo sapien		
16	61.6	529	4 Q9yz1	Q9yz1 homo sapien			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
No.	Score	Query Match	Length	DB ID	Description		
1	396.9	98.6	749	4 Q13433	Q13433 homo sapien		
2	353.2	88.0	765	11 Q8c145	Q8c145 mus musculus		
3	253.5	63.0	505	11 Q85118	Q85118 mus musculus		
4	228.0	56.7	433	4 Q8lxr3	Q8lxr3 homo sapien		
5	205.7	51.1	382	4 Q96ip5	Q96ip5 homo sapien		
6	133.7	33.2	835	4 Q9uef5	Q9uef5 homo sapien		
7	90.2	22.4	381	11 Q8bx42	Q8bx42 mus musculus		
8	787.5	19.6	701	5 Q9vsl7	Q9vsl7 drosophila		
9	73.4	18.2	528	6 Q9gv2	Q9gv2 macaca fasciata		
10	70.3	17.5	228	11 Q8c012	Q8c012 mus musculus		
11	657.5	16.3	539	4 Q8ny3	Q8ny3 homo sapien		
12	652.5	16.2	535	11 Q9db56	Q9db56 mus musculus		
13	652.5	16.2	535	11 Q9d09	Q9d09 mus musculus		
14	640	15.9	489	11 Q8ydl0	Q8ydl0 mus musculus		
15	63.7	15.7	531	4 Q1543	Q1543 homo sapien		
16	61.6	529	4 Q9yz1	Q9yz1 homo sapien			
SYNSEPTISTYNTVSEGHENLTETPRPGKLFLKDPSSTPSVTSKRSVSLRAGKT							
No.	Score	Query Match	Length	DB ID	Description		
1	396.9	98.6	749	4 Q13433	Q13433 homo sapien		
2	353.2	88.0	765	11 Q8c145	Q8c145 mus musculus		
3	253.5	63.0	505	11 Q85118	Q85118 mus musculus		
4	228.0	56.7	433	4 Q8lxr3	Q8lxr3 homo sapien		
5	205.7	51.1	382	4 Q96ip5	Q96ip5 homo sapien		
6	133.7	33.2	835	4 Q9uef5	Q9uef5 homo sapien		
7	90.2	22.4	381	11 Q8bx42	Q8bx42 mus musculus		
8	787.5	19.6	701	5 Q9vsl7	Q9vsl7 drosophila		
9	73.4	18.2	528	6 Q9gv2	Q9gv2 macaca fasciata		
10	70.3	17.5	228	11 Q8c012	Q8c012 mus musculus		
11	657.5	16.3	539	4 Q8ny3	Q8ny3 homo sapien		
12	652.5	16.2	535	11 Q9db56	Q9db56 mus musculus		
13	652.5	16.2	535	11 Q9d09	Q9d09 mus musculus		
14	640	15.9	489	11 Q8ydl0	Q8ydl0 mus musculus		
15	63.7	15.7	531	4 Q1543	Q1543 homo sapien		
16	61.6	529	4 Q9yz1	Q9yz1 homo sapien			
181 SYNSEPTISTYNTVSEGHENLTETPRPGKLFLKDPSSTPSVTSKRSVSLRAGKT							
No.	Score	Query Match	Length	DB ID	Description		
1	396.9	98.6	749	4 Q13433	Q13433 homo sapien		
2	353.2	88.0	765	11 Q8c145	Q8c145 mus musculus		
3	253.5	63.0	505	11 Q85118	Q85118 mus musculus		
4	228.0	56.7	433	4 Q8lxr3	Q8lxr3 homo sapien		
5	205.7	51.1	382	4 Q96ip5	Q96ip5 homo sapien		
6	133.7	33.2	835	4 Q9uef5	Q9uef5 homo sapien		
7	90.2	22.4	381	11 Q8bx42	Q8bx42 mus musculus		
8	787.5	19.6	701	5 Q9vsl7	Q9vsl7 drosophila		
9	73.4	18.2	528	6 Q9gv2	Q9gv2 macaca fasciata		
10	70.3	17.5	228	11 Q8c012	Q8c012 mus musculus		
11	657.5	16.3	539	4 Q8ny3	Q8ny3 homo sapien		
12	652.5	16.2	535	11 Q9db56	Q9db56 mus musculus		
13	652.5	16.2	535	11 Q9d09	Q9d09 mus musculus		
14	640	15.9	489	11 Q8ydl0	Q8ydl0 mus musculus		
15	63.7	15.7	531	4 Q1543	Q1543 homo sapien		
16	61.6	529	4 Q9yz1	Q9yz1 homo sapien			

Query Match	63.0%	Score 2533.5; DB 11; Length 505;	QY	396 MEMKRGPLFSLSSQNLEESAYFDSTWKGLTALGGLYFMFLYVHTLKFQFDKKKKNQ 455
Best Local Similarity	94.5%	Pred No. 5_5e-193;	Db	121 MEMKRGPLFSLSSQNLEESAYFDSTWKGLTALGGLYFMFLYVHTLKFQFDKKKKNQ 180
Matches 477; Conservative 13; Mismatches 14; Indels 1; Gaps 1;				
252 MYSRNTNENPOCPRASKLITSHGMGQVPLNATEBYNLCPATINOIDARSLCLHT -SEK 310	QY	456 KKPENDDVEIKKQLSKYESOLSTNEEKYTDDRTEGYLRADSQEPHSFDSQOPAVLEE 515		
1 MYSRNTNDNIOECRFTKLITSHGMQALLNATEBYNLCPATINOIDARCLHTASEK 60	Db	181 KKPENDDVEIKKQLSKYESOLSTNEEKYTDDRTEGYLRADSQEPHSFDSQOPAVLEE 240		
311 KAPIPKTYSLQIAWGGFIAISIISPLSLIGVILPMLNRVFFKELISPLVALAVGTLIS 370	QY	516 EYMIAHAAPOEVNEYTPRGCKNKCHSHPHDTQSDDLIHHHDYHHTLHHHHHQNHHP 575		
61 KAPIPKTYSLQIAWGGFIALISIISPLSLIGVILPMLNRVFFKELISPLVALAVGTLIS 120	Db	241 EYMIAHAAPOEVNEYTPRGCKNKCHSHPHDTQSDDLIHHHDYHHTLHHHHHQNHHP 300		
371 GDAFLHLLPHASHHHSHSREPAMENKROPLFSLHSQNLEESAYFDSTWKGLTALGG 430	QY	576 HSRSORYSRSEELKDAGTATLAWMVIDGHLNFNSDGLAIGAFTBLSGLSLSTSVAECH 635		
121 GDALHLLPHASHHHSHSREPAMENKROPLFSLHSQNLEESAYFDSTWKGLTALGG 30	Db	301 HSRSORYSRSEELKDAGTATLAWMVIDGHLNFNSDGLAIGAFTBLSGLSLSTSVAECH 360		
431 LYMFILYEHVHTLKLQFKDKKKKKNQKPPENDDVEIKKQLSKYESOLSTNEEKYTDDRTE	QY	636 ELPHELGDPAVLKLKGMTVKQAVLYNALSAMLAYLGMATGFIGHYAENYSMVFATAG 695		
181 LYMFILYEHVHTLKLQFRDKKKKKNQKPPENDDVEIKKQLSKYDSQLSNEKVDPGERP 240	Db	361 ELPHELGDPAVLKLKGMTVKQAVLYNALSAMLAYLGMATGFIGHYAENYSMVFATAG 420		
491 EGYLRAIDSQEPHSFQSQQPEVLEEEETMIAFHPOEVNEYTPRGCKNKCHSHFDITLGQ 550	QY	696 LFMYTAIVDMV 706		
241 ESYLRAIDSQEPHSFQSQQPEVLEEEETMIAFHPOEVNEYTPRGCKNKCHSHFDITLGQ 300	Db	421 LFMYTAIVDMV 431		
551 SDDLIIEHHHDYHILJAHHHHHNHPHSHSQYSRSEELKNAVGTLMAVINGDGLHNFNSD 610	QY	RESULT 5		
301 SDDLIIEHHHDYHILJAHHHHHNHPHSHSQYSRSEELKNAVGTLMAVINGDGLHNFNSD 360	Db	Q96HP5 PRELIMINARY; PRT; 382 AA.		
611 GLAIGAAFTEGLSSGLSTSVAECPHELGFAYVLKAGMFVKQAVLNALSAMLAYL 670	QY	AC Q96HP5; PRT; 382 AA.		
361 GLAIGAAFTEGLSSGLSTSVAECPHELGFAYVLKAGMFVKQAVLNALSAMLAYL 420	Db	DT 01-DEC-2001 (TREMBREL. 19, Created)		
671 GMATGIGTGHYAENYSMWFALTAGEMYALVDMPEMHLANDASDGCSERWGZFLQNA 730	QY	DT 01-MAR-2003 (TREMBREL. 23, Last sequence update)		
421 GMATGIGTGHYAENYSMWFALTAGEMYALVDMPEMHLANDASDGCSERWGZFLQNA 480	Db	DE Hypothetical protein (Fragile).		
731 GMILGFIMILLISITPEHKIVERNF 755	QY	OS Homo sapiens (Human).		
481 GMILGFIMILLISITPEHKIVERNF 505	Db	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;		
SEQUENCE FROM N.A.	RN	OX [1]		
RC TISSUE-Eye;	RP	RN		
Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.	RA			
EMBL; BC006317; AR08317; -	RL			
DR InterPro: IPR03639; Zn_transpt_Zip.	DR			
PFam: PF0535; Zip; 1.	DR			
KW Hypothetical protein.	KW			
NON_TER 1	FT			
SEQUENCE 382 AA; 43404 MW; AE4AE1C04401CDCB CRC64;	SQ			
Query Match 51.1%; Score 2057; DB 4; Length 382;				
Best Local Similarity 100.0%; Pred. No. 3 1e-155; Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
SEQUENCE FROM N.A.	RA			
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.	DR			
EMBL; BC039498; AAH9498.1; -	DR			
SEQUENCE 433 AA; 48650 MW; 72BBB90BDOA1867B CRC64;	SQ			
Query Match 56.7%; Score 2280; DB 4; Length 433;				
Best Local Similarity 100.0%; Pred. No. 6_6e-173; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
SEQUENCE FROM N.A.	RA			
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.	DR			
EMBL; BC039498; AAH9498.1; -	DR			
SEQUENCE 433 AA; 48650 MW; 72BBB90BDOA1867B CRC64;	SQ			
Query Match 276 MGIQVPLNATEFYNLCPATINOIDARSLCLHTSEKKAEPKRYSLQIAWGGFTAISI 335	QY	494 LRADSQEPHSFDSQQPAVLEEEVMAHAHPQEYVNEYVPRGCKNKCHSHFDITLGQSDD 553		
1 MGIQVPLNATEFYNLCPATINOIDARSLCLHTSEKKAEPKRYSLQIAWGGFTAISI 60	Db	1 FLHLLPHASHHHHSHEEPAMENKROPLFSLHSQNLEESAYFDSTWKGLTALGGYF 60		
336 SELSLGVLYPMVIMARVEPKELLSIYALVGTLSGDAFHLLPHASHHHSHSHEPA 395	QY	434 MFLVEHVLKLQFKDKKKKKQKPPENDDVEIKKQLSKYESQLSTNEEKYTDDRTEGY 493		
61 SELSLGVLYPMVIMARVEPKELLSIYALVGTLSGDAFHLLPHASHHHSHSHEPA 120	Db	61 FLHLLPHASHHHHSHEEPAMENKROPLFSLHSQNLEESAYFDSTWKGLTALGGYF 120		
Query Match 374 FLHLLPHASHHHHSHEEPAMENKROPLFSLHSQNLEESAYFDSTWKGLTALGGYF 433	QY	554 LHRRHHHDYHILHHHHHHONHHPHSHSQYRSREELKDAGVATLAWMYIMDGHLNFNSGCA 613		
Best Local Similarity 100.0%; Pred. No. 6_6e-173; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	121 LRADSQEPHSFDSQQPAVLEEEVMAHAHPQEYVNEYVPRGCKNKCHSHFDITLGQSDD 180		
SEQUENCE FROM N.A.	RA			
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.	DR			
EMBL; BC039498; AAH9498.1; -	DR			
SEQUENCE 433 AA; 48650 MW; 72BBB90BDOA1867B CRC64;	SQ			
Query Match 614 IGAATTEGLSSGLSTSTAVFCHELPELGFDFAVLKGMTVKQAVLYNALSAMIAYLGM 673	QY	181 LHRRHHHDYHILHHHHHHONHHPHSHSQYRSREELKDAGVATLAWMYIMDGHLNFNSGCA 240		
61 IGAATTEGLSSGLSTSTAVFCHELPELGFDFAVLKGMTVKQAVLYNALSAMIAYLGM 300	Db	241 IGAATTEGLSSGLSTSTAVFCHELPELGFDFAVLKGMTVKQAVLYNALSAMIAYLGM 300		

QY	535	GCKNKCHSH-FHDTLGOSDDDLIHHHHHDYHH-LHLLLHHQNHH--PFSHSQYSRSEELKD	589	RN	[2]
Db	166	--IHHEVHT-----SHHHDEDKAVLRSKGLAATFGLSSLSLSTAVTCHELPHELGDFAVLKK	213	RP	SEQUENCE FROM N.A.
QY	590	AGVATLAWNTNGDGLHNFSDGLAATGAFFGLSSLSLSTAVTCHELPHELGDFAVLKK 649	RA	RP	Adams M.D., Krommiller B., Wan K.H., Holt R.A., Celinker S.E., Gocayne J.D., Ananatides P.G., Branion R.C., Rogers Y., Evans C.A., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champ M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresen D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Hoskins R.A., Hostin D., Howland T.J., Ibeaweh C., Jalali M., Kruse D., Li P., Mattei B., Moskrafi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stabenow M., Strong R., Svirska R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
QY	650	AGMTVKQAVLYNALSAMLAYLGMAUTIGTGHAYENSMWIFALTAGLMVALDAYPEM 709	RA	RN	[3]
Db	274	AGMKVKQAVLYNALSAMLAYLGMAUTIGTGHAYENSMWIFALTAGLMVALDAYPEM 333	RA	RP	SEQUENCE FROM N.A.
QY	710	LHNDAA-SDHGSRSRGGFPLQNAGMLSEGMLISFEKIVRINF 755	RA	RA	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hrabecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Bernick B., Carlson J.W., Ceiniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
QY	334	LHGDDHEHGGCPYQEFQLQNLGILESPAMVIAVEKIVDQE 381	RA	RN	[4]
Db	301	FOI OR C66817.	RA	RP	SEQUENCE FROM N.A.
GN	OS	Drosophila melanogaster (Fruit fly).	RA	RA	Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
OC	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;	RA	RN	[5]
OC	OC	Ephydrioidea; Drosophilidae; Drosophila.	RA	RP	SEQUENCE FROM N.A.
OX	OX	NCBI_TAXID=7227;	RA	RA	Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
RN	[1]	SEQUENCE FROM N.A.	RA	RN	SEQUENCE FROM N.A.
RP	RESULT 8	STRAIN=Berkeley; MEDLINE=20190006; PubMed=10731132;	RA	RP	Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.
Q9VSL7	ID	Q9VSL7; PRELIMINARY; PRTE; 701 AA.	RA	RL	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards A., Ashburner M., Henderson S.N., Sutton G.G., Wormian J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champ M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Heit G., Andrews-Pfannkoch C., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballivet R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Bernier D.P., Bhandaari D., Bolshakov S., RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin R.J., Evangelista C.C., Ferrara C., Ferriera S., Fleischmann W., RA Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeaweh C., RA Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitus A.A., Pan S., Pollard J., Puriv V., Reese M.G., RA Reineke K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Sinden Kianos I., Simpson M.P., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirska R., Tector C., Turner E., Venter J., Wang X., RA Mount S.M., Moy M., Murphy L., Munday D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pollard J., Puriv V., Reese M.G., RA Reineke K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Sinden Kianos I., Simpson M.P., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirska R., Tector C., Turner E., Venter J., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhu S., Zheng L., RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000). RL

QY 405 SHLSISONIEESAYFDSTWKGLTALGGLYFMVHEHLLIKOF-KDKKKKKKKP--- 459
 Db 324 -----KGLCGLGIIFFYMEHALTMISERWSVKEKETKPKSRKV 365
 QY 460 -NDDDEIJKKQLS-----KYESOLSTNEEKYDIDDRTEGYLRAQSOPSHEDSQOPAV 511
 Db 366 MRDPDSVNNNSVAGDICKQKISSYCYDE-TIMNKQSENMLPFDYAAAGGDAFSV 424
 QY 512 LE-----EEEMYIAHARQEYNEYPRGCKNKCHSHHDHQSDDLI 555
 Db 425 AELRNGYGDHGSDNDMAAAASSLISPLHNCVERNHENKHNHSQNEE-GQDSNTI 482
 QY 556 -----HHHDYHILAHHHIONHDPHHSQRTSREELKDAGVATLW 597
 Db 483 VTDLDGNAYTAVNKAOKDSRDHYTIVLREHESHHIGHSH--RIGHVSPPELSSAWW 540
 QY 598 MVTMGDGLHNSFDSLTAIGAATFEGLSSGLTSVAFCHELPHELDFDFAVLLKAGMTYQA 657
 Db 541 MTTMGDGLHNTFDOMATGAARENNGFSTSLAVFCHELPHELDFDFALIKAGMSYSA 600
 QY 658 VLYNALSAMAYIYGMATCILFGHAYENNSWIAITGLXYVALDYMDPEMLHNDASDH 717
 Db 601 VYNNLTGVLISFTGMIIFARQ---SDVAQWMFAVAGLFITYIALYDMMPEI---SASH 655
 QY 718 GCSRNGYFFLQNAGMLGFGLMILLISIFE 746
 Db 656 --KSISQFLIQLIQIGLMSVGTMILALAYE 682

RESULT 9

Q96KV2 PRELIMINARY; PRT; 528 AA.
 ID .Q96KV2 PRELIMINARY; PRT; 528 AA.
 AC Q96KV2; DT 01-MAR-2001 ("TREMBLrel. 16, Created)
 DT 01-MAR-2001 ("TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 ("TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein 60.0 kDa protein
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecine; Macaca.
 RN [1] NCBI_TaxID=9541;
 RP SPOUSE FROM N.A.
 RC TISSUE=Cerebellum;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain CDNA
 libraries.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR AB01120; BAB18153.1; -.
 DR InterPro; IPRO03689; 2n_transpt_Zip.
 DR Pfam; PF0535; Zip; 1.
 SQ HYPOTHETICAL PROTEIN. SEQUENCE 528 AA; 60006 MW; E73669EC76580AAB CRC64;

Query Match 18.2%; Score 734; DB 6; Length 528;
 Best Local Similarity 32.7%; Pred. No. 8.9e-50;
 Matches 188; Conservative 89; Mismatches 188; Indels 110; Gaps 20;

QY 94 HDHDHSDHEHHSDHERHSDEHHSDHEHHSDHDDHHNHAAS---- 137
 Db 2 HDHHLRLHHLRH -HLD- HNNYHHEINDSTRPERGSENEPSTENKIQEQSVK 57

QY 138 ---GKMKRKALCPDHSD---SSGKDPRNSOGK----GAHRP-- HASGRNPKDSYAS 185
 Db 58 LPKGKMKKKRKSKNSNESEVTPGPNNHODQEYEHNVKPDYHNPGH----S 108

QY 186 EVTSVNTVSEGHTFLTETPRKPKDVSSPPSVTSKSRVSIAGKRTNEVS 245
 Db 109 HYHLPERNGHDPG-HGHQDLDPEDEGEL-----RHTRKREAPHYKNHII 152

QY 705 MPEPMHINDA--SDHGSCKSWGYFLQNGMGLGFGMLISIEHKIVFRNF 755
 Db 176 MLPEMLHGDDHEHGFCPCPYGOFTLQNLGLFGFAMLYVALVEDKLVDIOF 228

RESULT 10

Q8C0L2 PRELIMINARY; PRT; 228 AA.
 ID Q8C0L2 PRELIMINARY; PRT; 228 AA.
 AC Q8C0L2; DT 01-NER-2003 ("TREMBLrel. 23, Created)
 DT 01-NER-2003 ("TREMBLrel. 23, Last sequence update)
 DT 01-NER-2003 ("TREMBLrel. 23, Last annotation update)
 DE Weakly similar to CDNA FLJ32338 FIS (Fragment).
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Muridae; Murinae; Muridae; Murinae; Mus.
 RN [1] NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PUBMED=12466851;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK030685; BAC2/077.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 228 AA; 25075 MW; CEE696F7BEB544D6 CRC64;

Query Match 17.5%; Score 703; DB 11; Length 228;

Best Local Similarity 57.9%; Pred. No. 8.1e-48;
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 Db 4 HSH ----- SDGLETIHPHEBEVTSNHHDEDKAVLRKHSHOWHHRHHSGCHSG 55

QY 585 EELKDAYATLWVMTGDCOLHNFSGDAIGAATGEGLSSGLTSVAVCHELPHLGDF 644

Db 56 SDLKETGATLANTAWMYFMGDIAGAATGEGLSSGLTSVAVCHELPHLGDF 115

QY 645 AVLILKAGMTVKAOVLYNALSAMLAYLNATGIFIGHYANSMWVATLAGLFMYALVD 704
 Db 116 AVLILKAGTVKOAIVNLISAMMAYIGLIGAVGYYANNITLWIFATAGNEFLYALVD 175

QY 705 MPEPMHINDA--SDHGSCKSWGYFLQNGMGLGFGMLISIEHKIVFRNF 755

Db 176 MLPEMLHGDDHEHGFCPCPYGOFTLQNLGLFGFAMLYVALVEDKLVDIOF 228

protein - protein search, using sw model		September 12, 2003, 22:14:11 ; Search time 29 Seconds (without alignments) 1101.541 Million cell updates/sec			
Title: US-09-642-034-5		Last-processing: Minimum Match 0%			
Effect score: 4024	Quence: 1 MARKLSSVILITFALSIVNPI.....FGIMILISIFERKIVPRINF 755	Scoring table: BLOSUM62	Gapov 10.0 , Gapext 0.5		
Searched: 328717 seqs, 42310858 residues	Initial number of hits satisfying chosen parameters:	328717			
			minimum DB seq length: 0 maximum DB seq length: 2000000000		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		SUMMARIES			
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1	2205	54.8	431	1 US-09-311-023-2	Sequence 2 / Appl
2	3885	9.7	417	4 US-09-539-360A-88	Sequence 88 / Appl
3	166	4.1	450	4 US-09-663-600A-196	Sequence 196 / Appl
4	154	3.8	313	3 US-08-636-538A-3	Sequence 3 / Appl
5	154	3.8	313	3 US-09-456-287-3	Sequence 3 / Appl
6	154	3.8	337	3 US-08-686-538A-2	Sequence 2 / Appl
7	154	3.8	337	3 US-09-456-287-2	Sequence 2 / Appl
8	145	3.6	189	1 US-08-152-922A-6	Sequence 6 / Appl
9	143.5	3.6	185	2 US-08-758-621-4	Sequence 4 / Appl
10	143.5	3.6	355	3 US-09-107-838-4	Sequence 2 / Appl
11	140	3.5	309	1 US-09-161-406-2	Sequence 2 / Appl
12	138.5	3.4	167	3 US-09-507-333B-13	Sequence 13 / Appl
13	135	3.4	466	4 US-09-134-001C-749	Sequence 4749 / Appl
14	134	3.3	124	4 US-09-665-600A-102	Sequence 102 / Appl
15	134	3.3	339	4 US-09-328-35-6551	Sequence 6551 / Appl
16	132	3.3	363	4 US-09-328-352-4930	Sequence 4930 / Appl
17	127.5	3.2	448	3 US-09-446-474-8	Sequence 8 / Appl
18	124.5	3.1	474	3 US-09-461-474-10	Sequence 10 / Appl
19	123	3.1	275	4 US-09-134-001C-5540	Sequence 5540 / Appl
20	123	3.1	398	3 US-09-461-474-17	Sequence 17 / Appl
21	121	3.0	89	3 US-09-507-323B-12	Sequence 12 / Appl
22	121	3.0	349	3 US-09-461-474-12	Sequence 12 / Appl
23	121	3.0	649	2 US-09-490-09D-37	Sequence 37 / Appl
24	120.5	3.0	680	4 US-09-252-991A-29223	Sequence 29223 / Appl
25	120	3.0	368	1 US-08-211-945-17	Sequence 17 / Appl
26	119.5	3.0	726	3 US-09-416-482-2	Sequence 2 / Appl
27	119.5	3.0	726	3 US-09-416-482-2	Sequence 2 / Appl

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28	119.5	3.0	726	US-09-517-605-6
29	118	2.9	2509	US-08-149-097D-35
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32	116	2.9	1261	US-09-038-742-4
33	116	2.9	1261	US-09-032-295-2
34	116	2.9	1261	US-09-030-797-2
35	115.5	2.9	345	US-08-758-611-14
36	115.5	2.9	345	US-09-107-058-14
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38	115.5	2.9	339	US-09-107-058-12
39	113	2.8	707	US-09-134-001C-2962
40	112.5	2.8	344	US-09-134-001C-3524
41	111.5	2.8	765	US-08-063-112-2
42	111	2.8	535	US-08-007-107-2
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ALIGNMENTS

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 US-08-686-528A-3
 ; Sequence 3, Application US/08686528A
 ; GENERAL INFORMATION:
 ; Parent No. 6034134
 ; APPLICANT: LINGWOOD, Clifford A.
 ; TITLE OF INVENTION: HAEMOPHILUS ADHESIN PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
 ; STREET: 1737 King Street, Suite 500
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22314-2756
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/456, 287
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/686, 528
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rea, Teresa Stanek
 ; REGISTRATION NUMBER: 30, 427
 ; INFORMATION FOR SEQ ID NO: 3:
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/686, 528A
 ; FILING DATE: 26-JUL-1996
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rea, Teresa Stanek
 ; REGISTRATION NUMBER: 30, 427
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 313 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-686-528A-3

Query Match 3.8%; Score 154; DB 3; Length 313;
 Best Local Similarity 25.7%; Pred. No. 2.4e-06;
 Matches 54; Conservative 15; Mismatches 83; Indels 58; Gaps 7;

QY 84 IDEIKRITHH-DHDHSDEHHSDHHSHHNHDHHSHHNH---- 134
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 87 LSKAHHEHFEDGDHDHKHEHKHDHDHKHEKHDKHEHDDHHEGLTNW 146
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 QY 135 -----AASGKNRKALCPD----- 165
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 147 HWYSPATISKIVAQKDVKTAQFDKALIAONLSNRTAESEKITAQLANVKDKG 205
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 QY 166 AHRPHASSGRRNKVDVSASEVTSTVNT---VSEG---THRLETETPRPGKLFPKD 217
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 207 FYVFDAYGTEN----DAYGLQTKGFTINPLVAPGAKTIAKEEIDEKVNCFAAE- 260
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 QY 218 VSSSTPPSISVSKRSVSLAGRKTNEVSEP 247
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 261 -----PQFTPKVIESLAKNTKVNGQDP 284
 ; :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 6
 US-08-686-528A-2
 ; Sequence 2, Application US/08686528A
 ; Patent No. 6054134
 ; GENERAL INFORMATION:
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lingwood, Clifford A.
 ; STREET: 1737 King Street, Suite 500
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22314-2756
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/686, 528A

RESULT 5
 US-09-456-287-3
 ; Sequence 3, Application US/09456287
 ; Parent No. 6218147
 ; GENERAL INFORMATION:
 ; APPLICANT: LINGWOOD, Clifford A.
 ; TITLE OF INVENTION: HAEMOPHILUS ADHESIN PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.

FILING DATE: 26-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Rea, Teresa Stanek
 REGISTRATION NUMBER: 30-427
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 337 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-666-528A-2

Query Match Score 154; DB 3; Length 337;
 Best Local Similarity 25.7%; Pred. No. 2.7e-06;
 Matches 54; Conservative 15; Mismatches 83; Indels 58; Gaps 7;

Query Match Score 154; DB 3; Length 337;
 Best Local Similarity 25.7%; Pred. No. 2.7e-06;
 Matches 54; Conservative 15; Mismatches 83; Indels 58; Gaps 7;

Query 84 IDKIKRHHH--DHDHSDEHHSDHEHRSDEHHSDEHHSDHSHNH----- 134
 Db 111 LSAHAAHBFHEDGDHDHKHEKHDKHHDHDKHKAHEADHDHEGILTNW 170
 135 -----AASGKNNRKRAKCP----- 165
 Query 171 HWWSPAISSKIVAKQVADLTAQFDKKALIAQNLSDENRTLAQSKITAOQNLKDKG 230
 Db 166 AHPRHASGRNRVKDSVASETSTVNT---VSEG---TRFILETETPPGKLFPKD 217
 231 FYVFEHDAYGFN---DAYGLQTGETINPLVAGAKTLAKKEEDERYNCLEAF- 284

Query 84 IDKIKRHHH--DHDHSDEHHSDHEHRSDEHHSDEHHSDHSHNH----- 134
 Db 111 LSAHAAHBFHEDGDHDHKHEKHDKHHDHDKHKAHEADHDHEGILTNW 170
 135 -----AASGKNNRKRAKCP----- 165
 Query 171 HWWSPAISSKIVAKQVADLTAQFDKKALIAQNLSDENRTLAQSKITAOQNLKDKG 230
 Db 166 AHPRHASGRNRVKDSVASETSTVNT---VSEG---TRFILETETPPGKLFPKD 217
 231 FYVFEHDAYGFN---DAYGLQTGETINPLVAGAKTLAKKEEDERYNCLEAF- 284

Query 218 VSSSTPPSVTSKSRVSLAGRKTNEVSSEP 247
 Db 285 -----PQFTPKVIESLAKNTKVNQQLDP 308

RESULT 8
 US-08-152-922A-6

Sequence 6, Application US/08152922A
 ; Patent No. 5.395614
 ; GENERAL INFORMATION:
 ; APPLICANT: Knapp, Bernhard
 ; ATTORNEY: Hundt, Erika
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/152,922A
 ; FILING DATE: 16-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/806,471
 ; FILING DATE: 13-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elraudi, Carol F.
 ; REGISTRATION NUMBER: 32,220
 ; REFERENCE/DOCKET NUMBER: 02481-1143-02000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 189 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-152-922A-6

Query Match Score 145.5; DB 1; Length 189;

Best Local Similarity 28.4%; Pred. No. 6.9e-06; Matches 29; Conservative 14; Mismatches 52; Indels 7; Gaps 2; Qy 91 HIIH --- DHDHSIDDBHSDHRSDEHHSDHEHSDDIDHH --- SHNHLASGRNKRK 143 Db 7 HAHHADAHHAADAHHAAYAHAAHAAADAHHAADAHHAADAHHA 66 Qy 144 ALCPDHDSDSSGKDPRNSOQGRGAPEHASGRNRYKDSVAS 185 Db 67 HAADAHHAADAHHAADAHHAADAHHAADAHHAADAHHA 108

RESULT 9

; Sequence 4, Application US/08758621
; Patent No. 5846621
; GENERAL INFORMATION:
; APPLICANT: Guerinot, Mary Lou, and Eide, David J.
; TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/7758, 621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,578
; FILING DATE: 29-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: DCI-099CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-5941
; TELEFAX: (617)227-7400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; US-08-758-621-4

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 264 CENAKLITSHNGKIQPLNATEFYKLCAINOID---ARSCLIH ---TSEKKKEIPP 316 Db 6 CFSATMLR ---ICVVLICLICRCCASSDCNSHDPPSODEAKAT 48

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 317 KTY - SLQIAWVGFAISIISLGLVLPIM- NRVFKEFLLSFLVALAVGJSGD 372 Db 49 KKLGSSTALLVAGGVYS ---LPLIGRIPALQPNDIFF ---MYKFAVGLCT 99

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 373 AFLHLPHSHASHRHSHERPAMMKRGPFLSHSQNIEESAYFSTWKG ---LTAL 428 Db 100 GFVHILPDA ---FERLSSPCLEDITAGKFPPGFYVMLSAM 137

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 428 GGLYMFLEVYLTVLTIQFKDKKKNNQPKENDDDVKKLQSKTESQSLSTNEKVYDID 488 Db 138 GTLMF ---DT 144

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 489 RTEGYLRADSOEPHSQDQPAVLEEEVMIAHAPQEYVNEYVPRCKNKCHSHFHDTL 548 Db 145 FATEGYKQRQFSSNNNGSKQNYVDEE --- 172

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 549 QSDDLIHHHHDYHIIHHHHONH - PHHSQRYSRREELKDAGVATLAWVINGDGLHN 607 Db 173 ---VHTHTASHGHTGSTEILRR ---IVSOYLEGIVVHS 212

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 608 FSDGLAAGAETEGLSGLSTSVAFCHELPHELGDFAVLKGAGTVQANLYNALSMI 667 Db 213 VIIGISLGA --SQTDTIKPLMAALSFHOFEGLGGCISLADMKSSTVLMATFFSYT 270

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 668 ATYLMATGIG ---FIGHTAEN ---VSMTFALTAGEMYALVDRY ---PEMILHN 712 Db 271 APLIGIGGLCMSSGYKESKERIAYEGMUNASAGGLIXSYSLVLDATEDMPROSN 330

Query Match 3.6%; Score 143.5; DB 2; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 74; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 713 DASDHGSRNGYFFLQNA ---GMLGFGMILLISF 745 Db 331 ---LWLHAYLSLVLGAGSMSLLAW 354

RESULT 10

US-09-107-858-4

; Sequence 4, Application US/09107858
; Patent No. 6165900
; GENERAL INFORMATION:
; APPLICANT: Guerinot, Mary Lou et al.
; TITLE OF INVENTION: METAL REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPV
; CURRENT APPLICATION NUMBER: US/09/107, 858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758, 621
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 4
; SOFTWARE: Patentin Ver. 2.0
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-107-858-4

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 264 CFNASKLTSHGGMG1QVPLNATEFYKCPAIIQD---ARSCLIH ---TSEKKAEIIP 316 Db 6 CFSATMLR ---ICVVLICHMMCCASSTSIDDPYSQDAAEKAT 48

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 317 KTY - SLQIAWVGFIATISIISLGLVLPIM- NEVFFKEFLSFLVALANGTLSGD 372 Db 49 KKLGSSTALLVAGGVYS ---LPLIGRIPALQPNDIFF ---MVKAFAGVLLCT 99

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 373 AFLHLPHSHASHRHSHERPAMMKRGPFLSHSQNIEESAYFSTWKG ---LTAL 428 Db 100 GFVHILPDA ---FERLSSPCLEDITAGKFPPGFYVMLSAM 137

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 429 GGLYMFLEVYLTVLTIQFKDKKKNNQPKENDDDVKKLQSKTESQSLSTNEKVYDID 488 Db 138 GTLMF ---DT 144

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 489 RTEGYLRADSOEPHSQDQPAVLEEEVMIAHAPQEYVNEYVPRCKNKCHSHFHDTL 548 Db 145 FATEGYKQRQFSSNNNGSKQNYVDEE --- 172

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 549 QSDDLIHHHHDYHIIHHHHONH - PHHSQRYSRREELKDAGVATLAWVINGDGLHN 607 Db 173 ---VHTHTASHGHTGSTEILRR ---IVSOYLEGIVVHS 212

Query Match 3.6%; Score 143.5; DB 3; Length 355;
Best Local Similarity 18.6%; Pred. No. 3e-05; Mismatches 145; Indels 201; Gaps 20; Matches 96; Conservative 74; Mismatches 145; Indels 201; Gaps 20; Qy 608 FSDGLAAGAETEGLSGLSTSVAFCHELPHELGDFAVLKGAGTVQANLYNALSMI 667 Db 213 VIIGISLGA --SQTDTIKPLMAALSFHOFEGLGGCISLADMKSSTVLMATFFSYT 270

Page 6

RESULT 14
US-09-665-600A-102 ; Sequence 102, Application US/09663600A
Db 297 DNTNSLISRFR--QLANGAYKYN--PFLINQV 324 ;
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards , Jean-Baptiste
; APPLICANT: Bouquelier Lydie
; APPLICANT: Bouquelier Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED
; FILE REFERENCE: 31 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pmp
; SEO ID NO: 102

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; ORGANISM: Acinetobacter baumannii
US-09-328-352-6551

Query Match          3.3% ; Sco-
Best Local Similarity 29.1%; Pre-
Matches   32; Conservative 5; -
Qy      90 HTH-----HDH----DH
        :|: | | | | | | | | | | | |
Db      2 VKKHRYFEDYESSGHDDHNGRGGH
        | | | | | | | | | | | | | |
Qy      126 H---DHHSHHNRAASGKRNKRKA
        | | | | | | | | | | | | | |
Db      62 HLNDRDHHLRHH-----H
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Search completed: September 12, 2003,
Job time : 32 secs

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Query	Match	3.3%	Score 134;	DB 4;	Length 126;
Best Local Similarity	26.3%	Pred. No.	4.6e-05;		
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				Indels	38;
				Gaps	4;
Qy	1 MARKLSVLITLFALSVTNPFLHEKAAAAPQTEK-----ISPNWESGINVDLAIISTR 53				
Db	5 MHPFKCFLCLIFLTFIFHCNEIC EHDIQPEAHRLQRHGTMELIE-----SKFSKQAAINEK 60				
Qy	54 QTHLQLQFLYRIGENNNSLSVGEFKRLLONGIDIKRTHIHDHDHSDHEHSDHERHSD 113				
Db	61 KYYLEKLPERCENGRLSFGGLEKLNLNGLGFLERKVYEINHE-----102				
Qy	114 HEHHSDHPHSHDHHSHDHHSHNHAAGSKNKKAL 145				
Db	103 -----DYGHDHSHDHHSHDHHSHNHAAGSKNKKAL 125				

RESULT 15
US-09-328-352-6551
Sequence 651, Application US/09328352
Patent No. 6562458
GENERAL INFORMATION:
APPLICANT: Gary L. Brereton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUDMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/3228, 352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOs: 8252
SEQ ID NO 6551
LENGTH: 339
TYPE: PRT

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OM protein - protein search, using sw model

Run on : September 12, 2003, 22:18:56 ; Search time 58 Seconds
(without alignments)

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	3969	98.6	749	15	US-10-177-283-264	Sequence 264 , App
2	3906	97.1	752	15	US-10-176-847-52	Sequence 52 , App
3	1972	49.0	397	10	US-09-923-300-1531	Sequence 1531 , Ap
4	1337	33.2	831	9	US-09-789-561-86	Sequence 86 , App
5	640	15.9	1232	12	US-10-017-161-2396	Sequence 2396 , Ap
6	543.5	13.5	647	11	US-09-965-529-16	Sequence 16 , Appl
7	543.5	13.5	647	11	US-09-965-680A-16	Sequence 16 , Appl
8	404	10.0	626	15	US-10-097-340-95	Sequence 95 , Appl
9	401.5	10.0	737	12	US-10-107-161-2394	Sequence 2394 , Ap
10	395.5	9.8	204	15	US-10-107-806-743	Sequence 743 , App
11	234	5.8	354	15	US-10-050-704-115	Sequence 115 , App
12	234	5.8	383	15	US-10-239-704-239	Sequence 239 , App
13	192	4.8	292	9	US-09-864-761-3794	Sequence 3794 , A
14	166	4.1	150	12	US-10-318-763-196	Sequence 196 , App
15	166	4.1	307	11	US-09-946-374-95	Sequence 95 , Appl

16	166	4.1	307	12	US-10-015-387A-95	Sequence 95 , Appl
17	166	4.1	307	12	US-10-179-672-262	Sequence 95 , Appl
18	166	4.1	307	12	US-10-006-172A-95	Sequence 95 , Appl
19	166	4.1	307	12	US-10-187-749-263	Sequence 262 , App
20	166	4.1	307	12	US-10-184-477-262	Sequence 262 , App
21	166	4.1	307	12	US-10-184-642-262	Sequence 262 , App
22	166	4.1	307	12	US-10-156-747-262	Sequence 262 , App
23	166	4.1	307	12	US-10-015-312A-95	Sequence 95 , Appl
24	166	4.1	307	12	US-10-017-233A-95	Sequence 95 , Appl
25	166	4.1	307	12	US-10-173-639-262	Sequence 262 , App
26	166	4.1	307	12	US-10-173-691-262	Sequence 262 , App
27	166	4.1	307	12	US-10-173-632-262	Sequence 262 , App
28	166	4.1	307	12	US-10-173-638-262	Sequence 262 , App
29	166	4.1	307	12	US-10-173-674-262	Sequence 262 , App
30	166	4.1	307	12	US-10-173-638-262	Sequence 262 , App
31	166	4.1	307	12	US-10-173-639-262	Sequence 262 , App
32	166	4.1	307	12	US-10-173-707-262	Sequence 262 , App
33	166	4.1	307	12	US-10-175-736-262	Sequence 262 , App
34	166	4.1	307	12	US-10-175-742-262	Sequence 262 , App
35	166	4.1	307	12	US-10-174-583-262	Sequence 262 , App
36	166	4.1	307	12	US-10-174-587-262	Sequence 262 , App
37	166	4.1	307	12	US-10-174-589-262	Sequence 262 , App
38	166	4.1	307	12	US-10-174-591-262	Sequence 262 , App
39	166	4.1	307	12	US-10-175-736-262	Sequence 262 , App
40	166	4.1	307	12	US-10-175-744-262	Sequence 262 , App
41	166	4.1	307	12	US-10-175-745-262	Sequence 262 , App
42	166	4.1	307	12	US-10-175-748-262	Sequence 262 , App
43	166	4.1	307	12	US-10-175-751-262	Sequence 262 , App
44	166	4.1	307	12	US-10-175-754-262	Sequence 262 , App
45	166	4.1	307	12	US-10-175-754-262	Sequence 262 , App

ALIGNMENTS

RESULT 1	US-10-177-293-264	; Sequence 264 , Application US/10177293
		; Publication No. US20030124128A1
		/ GENERAL INFORMATION:
		/ APPLICANT: Lille, James
		/ APPLICANT: Glatt, Karen
		/ APPLICANT: Zhao, Xumei
		/ APPLICANT: Ganavarpu, Mandula
		/ APPLICANT: Kamatkar, Shubhangi
		/ APPLICANT: Mertens, Maureen
		/ APPLICANT: Meyer, Vic
		/ APPLICANT: Wang, Youyao
		/ APPLICANT: Xu, Yongyao
		/ APPLICANT: Hoersch, Sebastian
		/ APPLICANT: Monahan, John
		/ APPLICANT: Meyers, Rachel E.
		/ APPLICANT: Bast Jr., Robert C.
		/ APPLICANT: Horobayi, Gabriel N.
		/ APPLICANT: Pusztai, Lajos
		/ APPLICANT: Meric, Funda
		/ APPLICANT: Sahn, Aysegul

Page 2

Sequence 1531, Application US/09925300
 Patent No. US20151681A1
 GENERAL INFORMATION:
 APPLICANT: Craig Rosen,
 APPLICANT: Steve Ruben
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05988
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1890
 SEQ ID NO: 1531
 SOFTWARE: Patentin Ver. 2.0
 LENGTH: 397
 TYPE: PAT
 ORGANISM: Homo sapiens
 NAME/KEY: SITE
 LOCATION: (179)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (180)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (181)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (358)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-09-925-300-1531

Query Match 49.0%; Score 1972; DB 10; Length 397;
 Best Local Similarity 98.7%; Pred. No. 1.5e-164;
 Matches 376; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

181 SYSAEVTSTVNTVSEGTHFLETTTPRKGKLFPKDVSSTPPSYTSKRSVSLAGRT 240
 1 SVSASEVTSTVNTVSEGTHFLETTTPRKGKLFPKDVSSTPPSYTSKRSVSLAGRT 60

QY 181 SYSAEVTSTVNTVSEGTHFLETTTPRKGKLFPKDVSSTPPSYTSKRSVSLAGRT 240
 1 SVSASEVTSTVNTVSEGTHFLETTTPRKGKLFPKDVSSTPPSYTSKRSVSLAGRT 60

Db 241 NEVSSEPRKGFMYSRNTENNPQECAFNSKULTSQHMGIQVNATENYLCPATINQIDA 300
 61 NEVSSEPRKGFMYSRNTENNPQECAFNSKULTSQHMGIQVNATENYLCPATINQIDA 120

QY 241 NEVSSEPRKGFMYSRNTENNPQECAFNSKULTSQHMGIQVNATENYLCPATINQIDA 300
 61 NEVSSEPRKGFMYSRNTENNPQECAFNSKULTSQHMGIQVNATENYLCPATINQIDA 120

Db 301 RSCLIHTSERKAEIPTPKYSLQIAWVGFIAISITSLGIVLTVPLMNRVFFKELLPSF 360
 121 RSCLIHTSERKAEIPTPKYSLQIAWVGFIAISITSLGIVLTVPLMNRVFFKELLXX 180

QY 301 RSCLIHTSERKAEIPTPKYSLQIAWVGFIAISITSLGIVLTVPLMNRVFFKELLPSF 360
 121 RSCLIHTSERKAEIPTPKYSLQIAWVGFIAISITSLGIVLTVPLMNRVFFKELLXX 180

361 IVALAYGTLSGDAFLHLPHASHHSHSHHEPAMEMKRGPFLSHLSSONIEESAYFDS 420
 181 XVALAYGTLSGDAFLHLPHASHHSHSHHEPAMEMKRGPFLSHLSSONIEESAYFDS 240

Db 361 IVALAYGTLSGDAFLHLPHASHHSHSHHEPAMEMKRGPFLSHLSSONIEESAYFDS 420
 181 XVALAYGTLSGDAFLHLPHASHHSHSHHEPAMEMKRGPFLSHLSSONIEESAYFDS 240

421 TWKGLTAIGGLYPMELVERLTLIKQFKDKKKNNKKPENDDVEIKKOLSKYEQSQLSTN 480
 241 TWKGLTAIGGLYPMELVERLTLIKQFKDKKKNNKKPENDDVEIKKOLSKYEQSQLSTN 300

QY 421 TWKGLTAIGGLYPMELVERLTLIKQFKDKKKNNKKPENDDVEIKKOLSKYEQSQLSTN 480
 241 TWKGLTAIGGLYPMELVERLTLIKQFKDKKKNNKKPENDDVEIKKOLSKYEQSQLSTN 300

481 EEKVDTDDRTGYLRADSOEPHSFDSQQAVLEEEVMTAHAHQPEVYNEYVPRGCKNKC 540
 301 EEKVDTDDRTGYLRADSOEPHSFDSQQAVLEEEVMTAHAHQPEVYNEYVPRGCKNKC 360

QY 481 EEKVDTDDRTGYLRADSOEPHSFDSQQAVLEEEVMTAHAHQPEVYNEYVPRGCKNKC 540
 301 EEKVDTDDRTGYLRADSOEPHSFDSQQAVLEEEVMTAHAHQPEVYNEYVPRGCKNKC 360

541 HSHFHDTLGQSDDLTHHHHDY 561
 361 HSHFHDTLGQSDDLTHHHHDY 381

Db 541 HSHFHDTLGQSDDLTHHHHDY 561
 361 HSHFHDTLGQSDDLTHHHHDY 381

554 PDSWDLQKPLAGTDQSVSSEDRNETETDLEGQOQSPPNYCIEEKIDHSHSDGL 613

528 YNEYVPRGCKNCKSHFHDTLGQSDDLTHHHHDYHHLHHHHQHMHSHQSQR--YSR 584
 614 HT-----IHFHDIIAAAH----NHGEENKTYTREHHWHHHSHGPHSG 658

585 BELKDAYATLAWMVMDGLHNFSDGLAIGAFTERSSLGSLSTSVAVFCHELPHELGDF 644
 659 SLDKETGIANIAWVMDGDIHNFSDGLAIGAFAHGSGLGGISISIAVFCHELPHELGDF 718

RESULT 4
 US-09-789-561-86
 Sequence 86, Application US/09789561
 Patent No. US200604818A1
 GENERAL INFORMATION:
 APPLICANT: Ni et al.

Page 6

QY 467 KQKLSKYESQLSTNEEKVDTDDRTEGYLRLADSQEFSHSDQSOPAVLLEEYMAAHAPQE 524
 QY : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 DB 208 AAALN------GGHCLAA-----QPA-----AEP----- 224
 QY 527 VNEYVPRGCKKNCKHSHFDLQGSDDLIHHHHYHHHHQNHHPHSHSQYRSRE 583
 Db 225 -----GIGA-----VVRS 234
 QY 587 LKDAGVATLAWAYTMDGLHNNSDGLAIGAAFTEGLSSGLSTSVAATCHELPHELGDFAV 641
 Db 233 : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 QY 647 LLKAGMTVKQAVLYNNALSMALYLNMTGIFTG-----HYADNVSHWTFALTAGI 694
 Db 288 ILRAG-----FDRISAAKQLSTALGGLLGAGFAICTQSXKGVEETAAWVLPTSGG 333
 QY 697 FMYVALDVKVPMEMLENDASDHGCSRNGYFLQNAQML-LGF3IMLISIF 745
 Db 340 FLYIALVNVLPDILDEE-----DPWR-----SLQQLLCAGIVVNLFSLF 381

RESULT 13
 US -09 -864 -761 -37944
 Sequence 37944, Application US/09864761
 Patent No. US20090048763A1
 GENERAL INFORMATION:
 APPLICANT: Fenn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanel, David K.
 APPLICANT: Chen, Wenshang
 TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES US
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-12-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24223.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,587
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117

; PRIOR APPLICATION NUMBER: 60/098750
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR FILING DATE: 1998-09-13
 ; PRIOR FILING DATE: 1998-09-13
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR FILING DATE: 1998-09-273
 ; PRIOR FILING DATE: 1998-09-04
 ; NUMBER OF SEQ ID NOS: 229
 ; SOFTWARE: Patent-PM
 ; SEQ ID NO: 196
 ; LENGTH: 150
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-319-763-196

Query Match 1
 Best Local Similarity 4.1%; Score 166; DB 12; Length 150;
 Matches 43; Conservative 27; Mismatches 66; Indels 12; Gaps 4;
 QY 1 MARKLIVVILTFPLSVALSYNPNLHEKAAFFPOTKEK-----LSPNWESGINVDIASTR 53
 Db 5 MHTKFCCLICLTFTPHCNHCHE-EHDHGPEALRHRQHGMTELP---SKESKQAENEK 60

QY 54 QYHQLQFLRYGENMNSLVEGERKLQNGIDTKRKHHDHHSDDHHSDHRS 113
 Db 61 KYXIERLFLRYGENRLSFGGLEKLULNLGLENKVVBINHDLGI-DYSHLGILAYQE 119

QY 114 HEHSDHEHSDHSDHSHHHADASGENRK 143
 Db 120 GKHFISHNQHSHHNLNSENQTVTSYSTKK 149

RESULT 15
 US-09-946-374-95
 Sequence 95, Application US/09946374
 Publication No. US20030073129A1
 GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillen, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Thomas, Daniel
 ; APPLICANT: Watanaabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C1
 ; CURRENT APPLICATION NUMBER: US/09/946,374
 ; CURRENT FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/101279

PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307
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PRIOR FILING DATE: 1998-09-29
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PRIOR FILING DATE: 1998-09-30
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PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711

PRIOR APPLICATION NUMBER:	60/1042547	Score:	4.1%
PRIOR FILING DATE:	1998-10-14	Priority:	
PRIOR APPLICATION NUMBER:	60/1049856	Priority:	
PRIOR FILING DATE:	1998-10-20	Priority:	
PRIOR APPLICATION NUMBER:	60/1050006	Priority:	
PRIOR FILING DATE:	1998-10-20	Priority:	
PRIOR APPLICATION NUMBER:	60/1050006	Priority:	
PRIOR FILING DATE:	1998-10-20	Priority:	
PRIOR APPLICATION NUMBER:	60/1051046	Priority:	
PRIOR FILING DATE:	1998-10-21	Priority:	
PRIOR APPLICATION NUMBER:	60/1051656	Priority:	
PRIOR FILING DATE:	1998-10-22	Priority:	
PRIOR APPLICATION NUMBER:	60/1052667	Priority:	
PRIOR FILING DATE:	1998-10-22	Priority:	
PRIOR APPLICATION NUMBER:	60/1056959	Priority:	
PRIOR FILING DATE:	1998-10-26	Priority:	
PRIOR APPLICATION NUMBER:	60/1056959	Priority:	
PRIOR FILING DATE:	1998-10-26	Priority:	
PRIOR APPLICATION NUMBER:	60/1058001	Priority:	
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Best Local Similarity:	24.8%	Score:	24.8%
Matches:	68;	Priority:	40;
		Priority:	
Qry		Priority:	
Dbx	532 VPRCKKNCHSHFHDLGQSDDLL 55 VPEG---VHALYDILEKG	Priority:	532 AFTBGLSSGLSTSVAVCHELPHPHI 55 ASTSOTSVOLIVVAIMLHKAPAH
Qry		Priority:	
Dbx	579 ---SQT 107 YIGTSVLGVFMNLVDQIGNSH	Priority:	670 LGW-----ATGIFTIGH 227 LGLSKSSXBALESBNMTGTV---
Qry		Priority:	
Dbx	617 AFTBGLSSGLSTSVAVCHELPHPHI 167 ASTSOTSVOLIVVAIMLHKAPAH	Priority:	715 SD---HGCSSRKGYFLQNAGMLI 275 PDTGGGRSLR---LEVAAVLT
Qry		Priority:	
Dbx	670 LGW-----ATGIFTIGH 227 LGLSKSSXBALESBNMTGTV---	Priority:	715 SD---HGCSSRKGYFLQNAGMLI 275 PDTGGGRSLR---LEVAAVLT